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**Stamatoyannopoulos et al.**

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(45) **Date of Patent:** **Jun. 7, 2022**

(54) **METHODS FOR FLUORESCENCE IMAGING MICROSCOPY AND NANO-FISH**

(2013.01); *G01N 21/6458* (2013.01); *G01N 21/78* (2013.01); *G01N 33/56966* (2013.01); *G01N 33/574* (2013.01); *G01N 33/582* (2013.01); *C40B 30/04* (2013.01); *G01N 2015/0038* (2013.01)

(71) Applicant: **Altius Institute for Biomedical Sciences, Seattle, WA (US)**

(58) **Field of Classification Search**  
CPC ..... *G01N 21/64*; *C12N 5/0694*; *C12Q 1/6841*  
See application file for complete search history.

(72) Inventors: **John A. Stamatoyannopoulos, Seattle, WA (US); Shreeram Akilesh, Seattle, WA (US); Vivek Nandakumar, Seattle, WA (US)**

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(73) Assignee: **Altius Institute for Biomedical Sciences, Seattle, WA (US)**

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(\* ) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 70 days.

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(21) Appl. No.: **16/319,157**

(22) PCT Filed: **Jul. 19, 2017**

(86) PCT No.: **PCT/US2017/042946**

§ 371 (c)(1),

(2) Date: **Jan. 18, 2019**

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(87) PCT Pub. No.: **WO2018/017774**

PCT Pub. Date: **Jan. 25, 2018**

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(65) **Prior Publication Data**

US 2019/0234881 A1 Aug. 1, 2019

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**Related U.S. Application Data**

(60) Provisional application No. 62/364,245, filed on Jul. 19, 2016.

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GenBank data sheet, H1N1 Influenza segment 5, printed on Aug. 21, 2020, pp. 1-2 (Year: 2020).\*  
GenBank data sheet, H1N1 Influenza segment 6, printed on Aug. 20, 2020, pp. 1-2 (Year: 2020).\*  
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Raj et al., (2008) "Imaging individual mRNA molecules using multiple singly labeled probes," *Nature Methods*, 5(10):877-879.

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(51) **Int. Cl.**

<i>G01N 21/64</i>	(2006.01)
<i>C12Q 1/6841</i>	(2018.01)
<i>C40B 40/06</i>	(2006.01)
<i>G01N 21/78</i>	(2006.01)
<i>G01N 33/574</i>	(2006.01)
<i>G01N 33/58</i>	(2006.01)
<i>G01N 33/569</i>	(2006.01)
<i>A01N 1/02</i>	(2006.01)
<i>C12N 5/078</i>	(2010.01)
<i>C12N 5/09</i>	(2010.01)
<i>C12P 19/34</i>	(2006.01)
<i>G01N 1/30</i>	(2006.01)
<i>C12Q 1/6837</i>	(2018.01)
<i>C40B 30/04</i>	(2006.01)
<i>G01N 15/00</i>	(2006.01)

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(52) **U.S. Cl.**

CPC ..... *G01N 21/64* (2013.01); *A01N 1/0221* (2013.01); *C12N 5/0634* (2013.01); *C12N 5/0694* (2013.01); *C12P 19/34* (2013.01); *C12Q 1/6837* (2013.01); *C12Q 1/6841* (2013.01); *C40B 40/06* (2013.01); *G01N 1/30*

(57) **ABSTRACT**

Disclosed herein are methods of detecting a target nucleic acid sequence, determining the localization of the target nucleic acid sequence, and/or quantifying the number of target nucleic acid sequences in a cell. This method may be used on small target nucleic acid sequences, and may be referred to as Nano-FISH.

**14 Claims, 39 Drawing Sheets**

**Specification includes a Sequence Listing.**

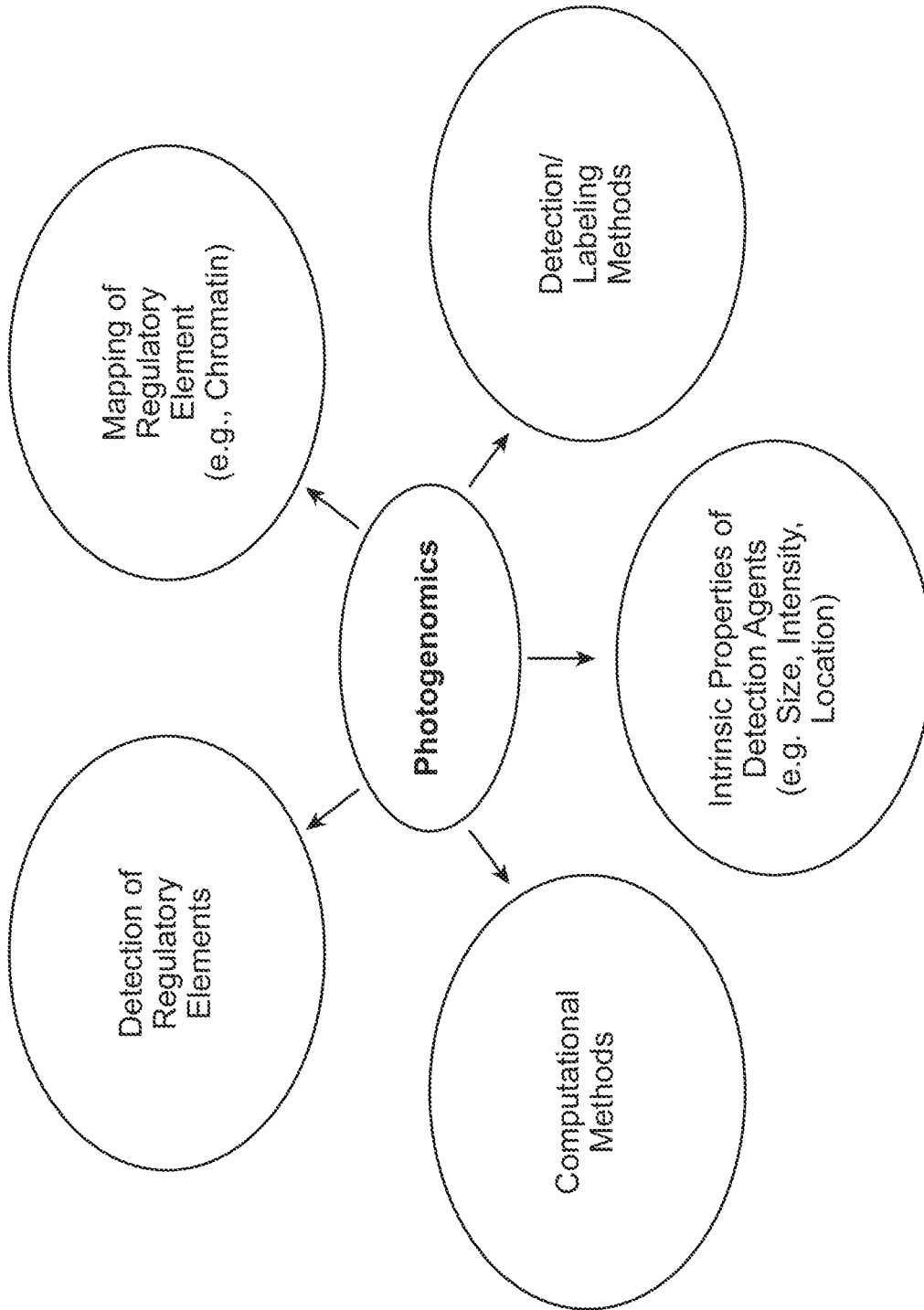


FIG. 1

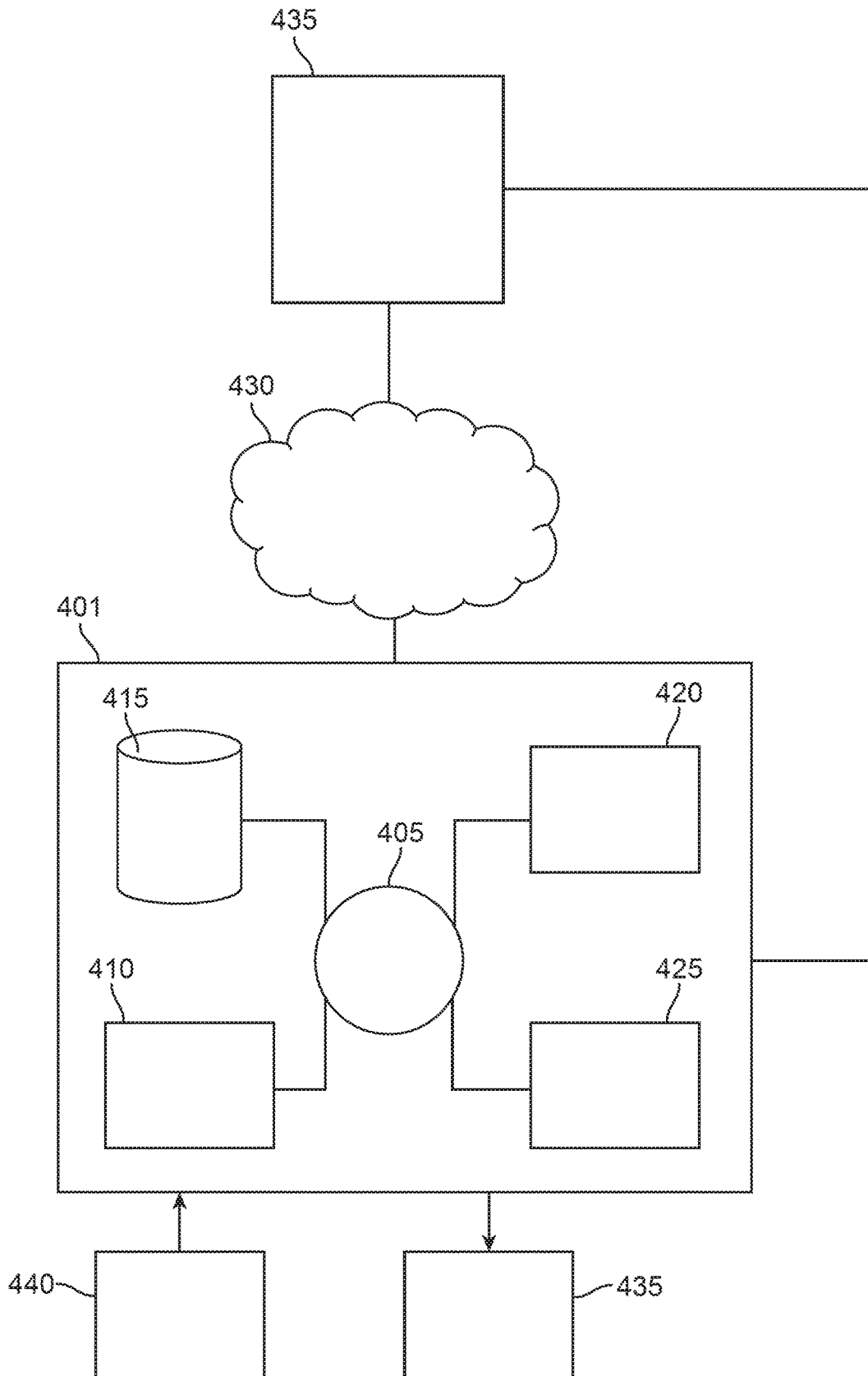


FIG. 2

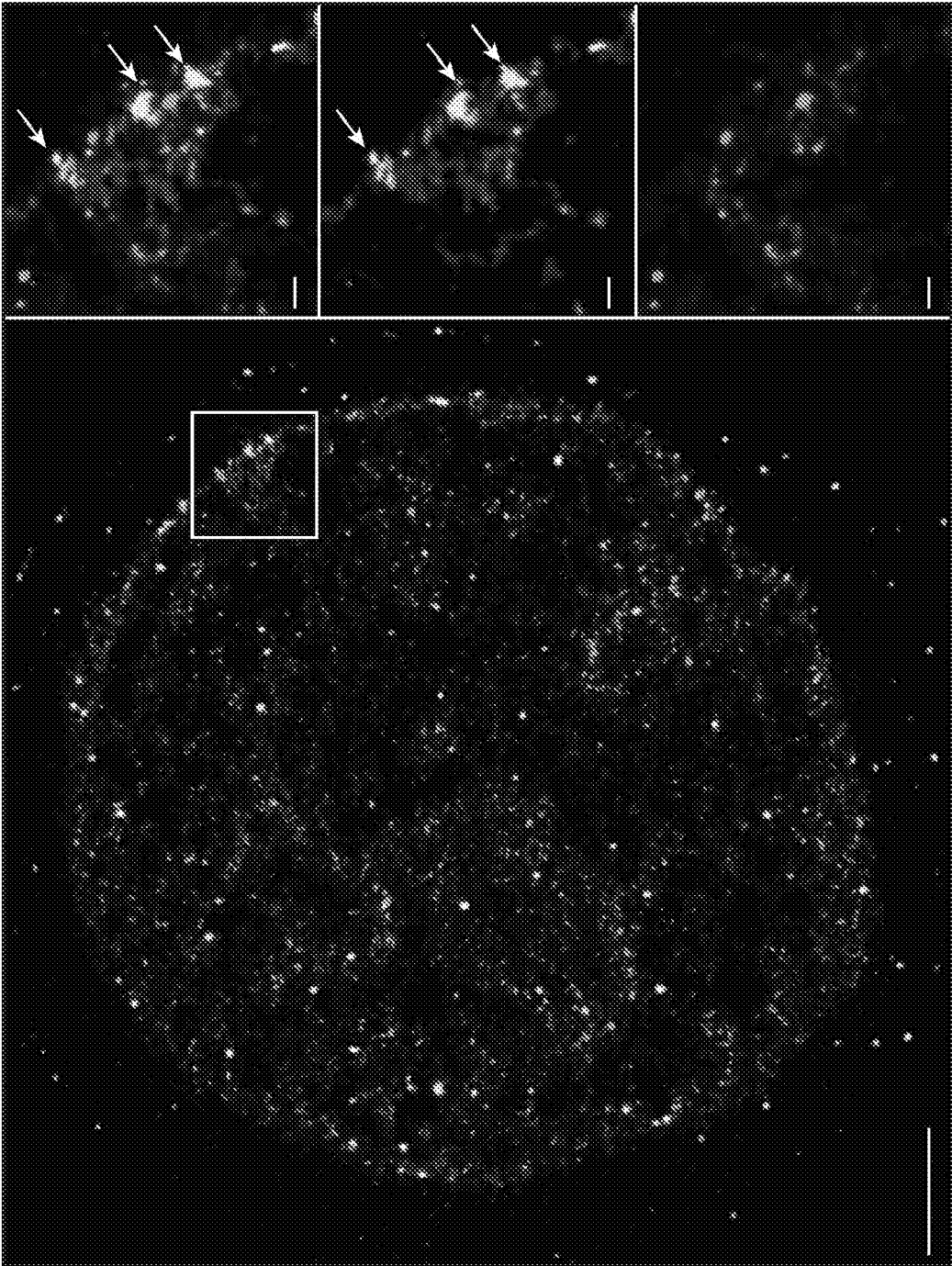


FIG. 3A

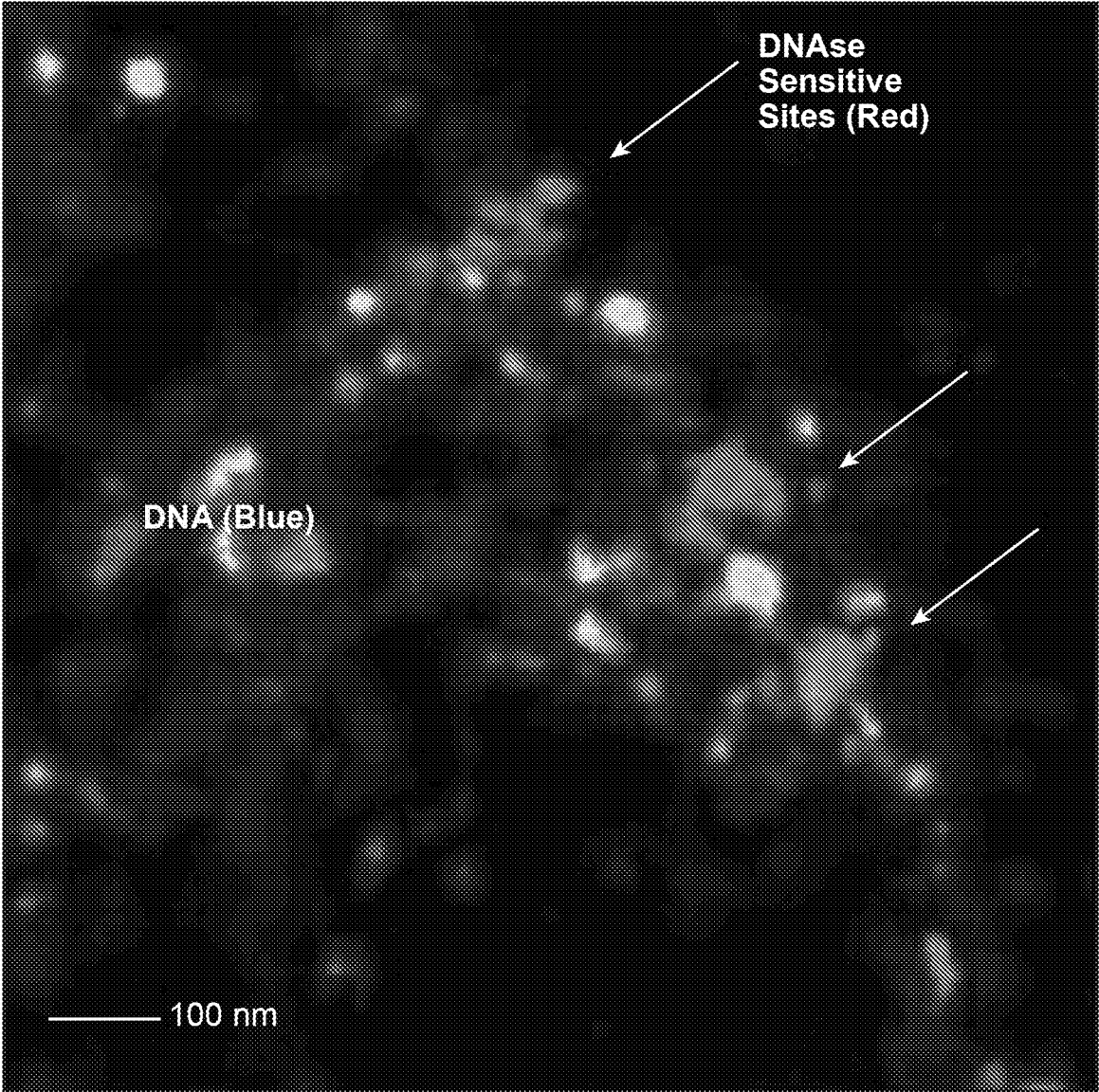


FIG. 3B

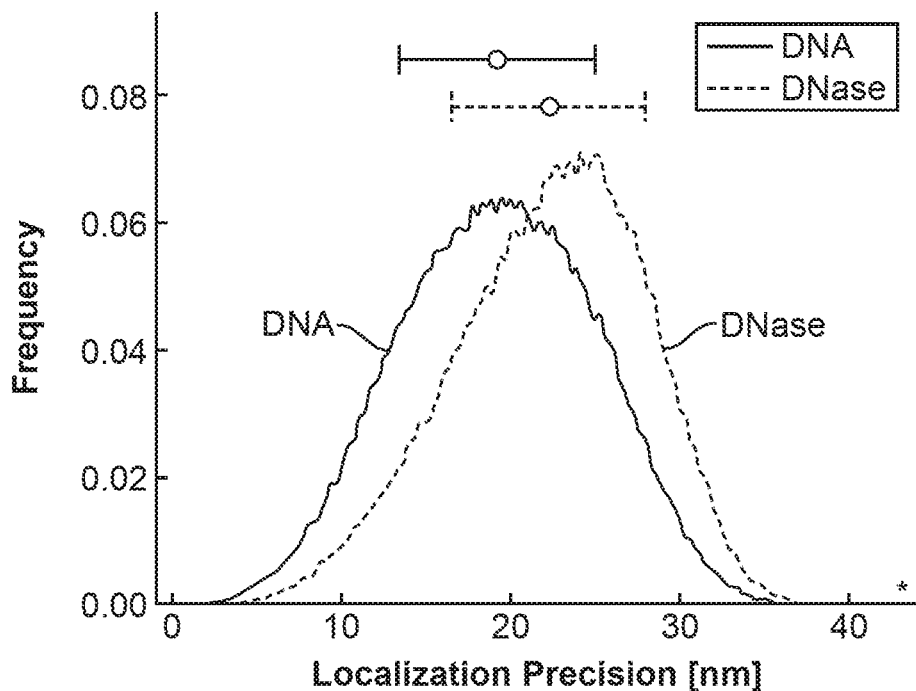


FIG. 4A

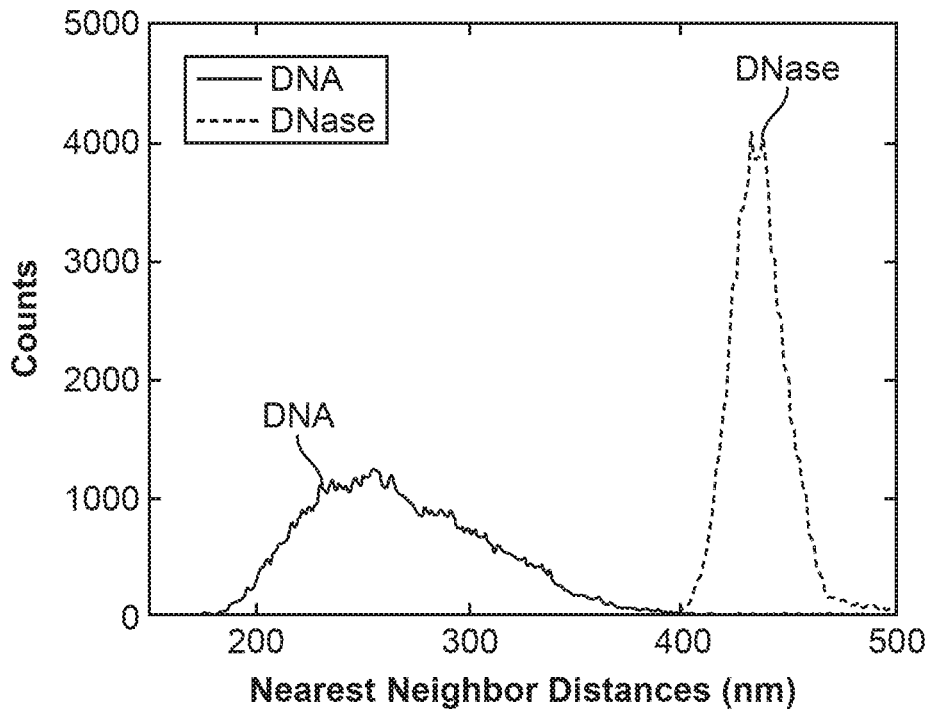
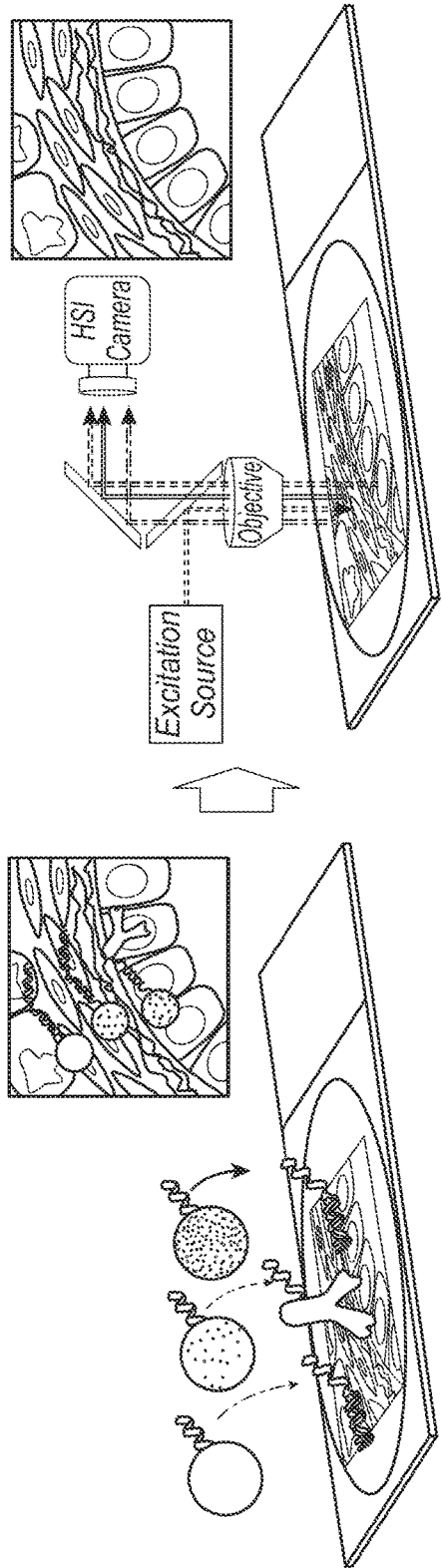


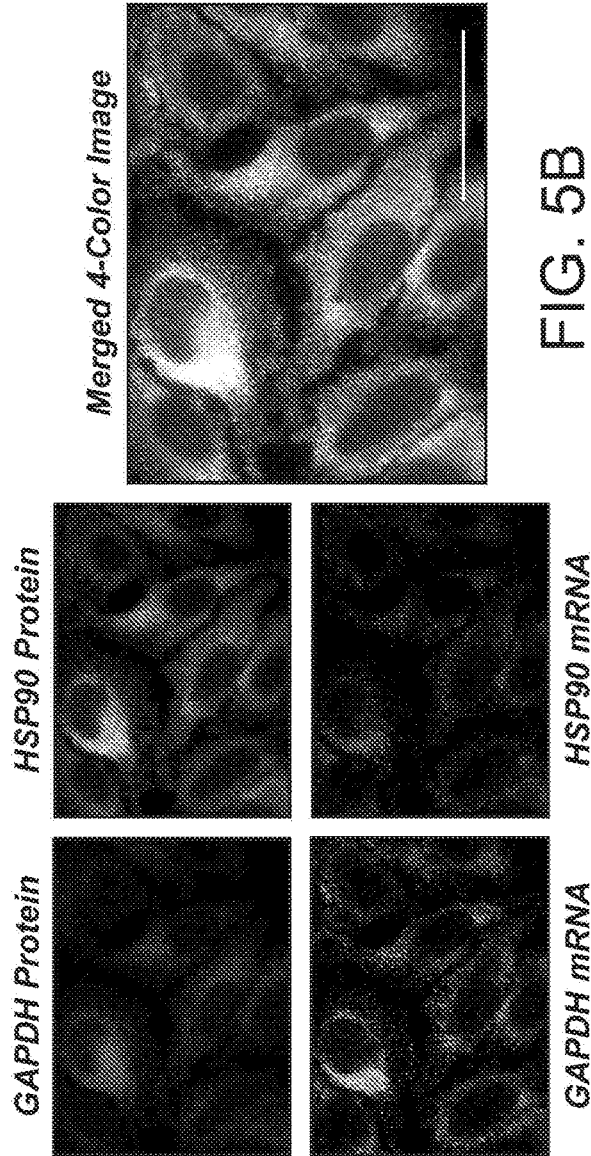
FIG. 4B



*Multiplexed Imaging*

**FIG. 5A**

*Specimen Labeling with QDots*



**FIG. 5B**

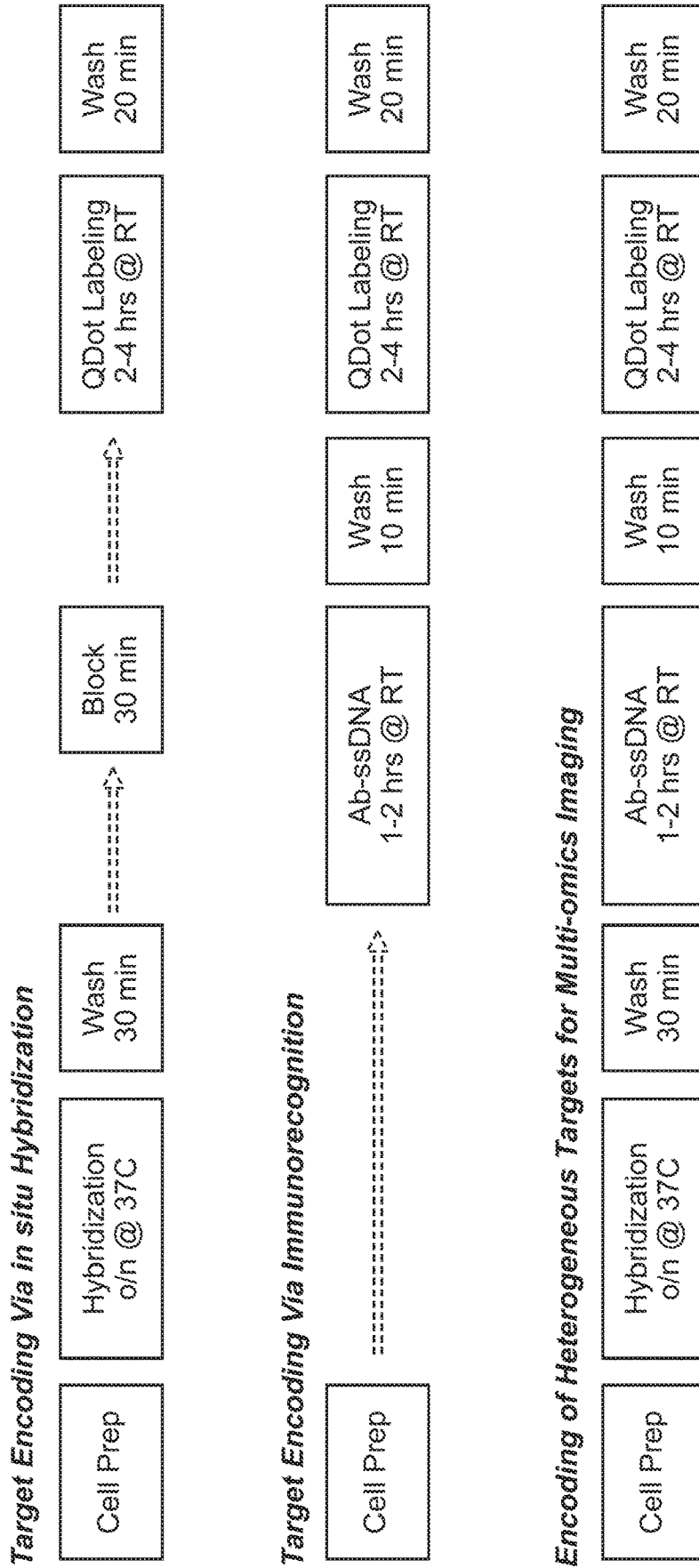


FIG. 6

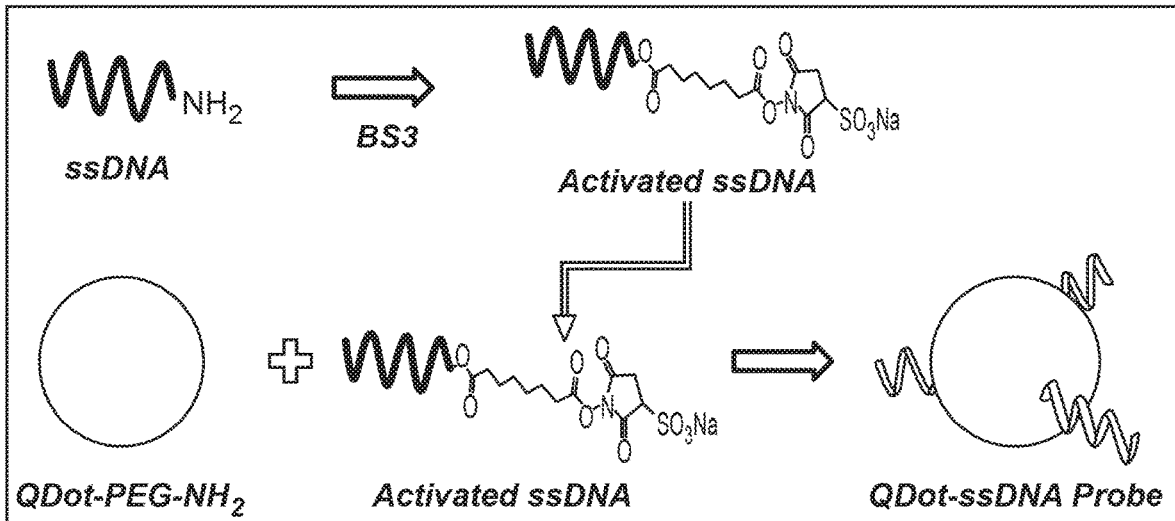


FIG. 7A

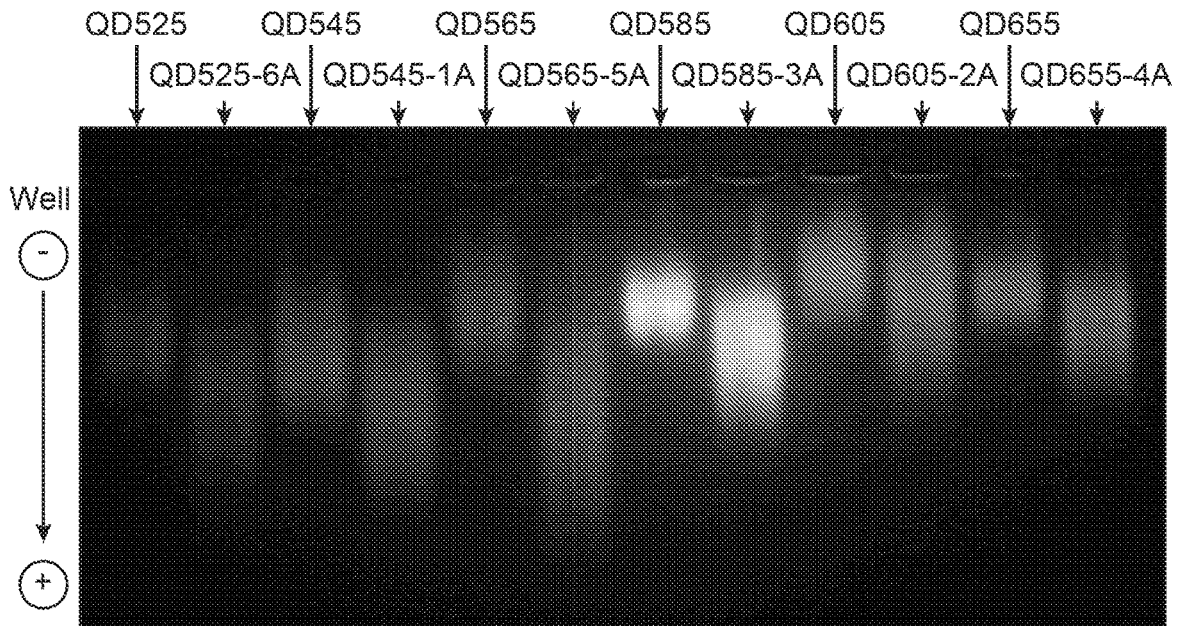


FIG. 7B

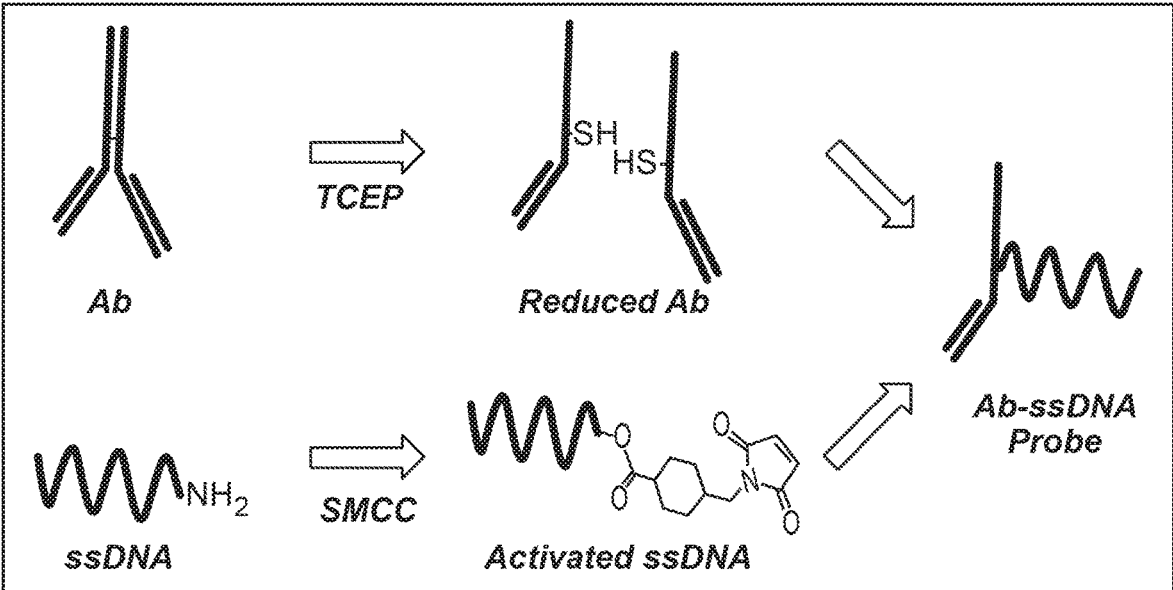


FIG. 8A

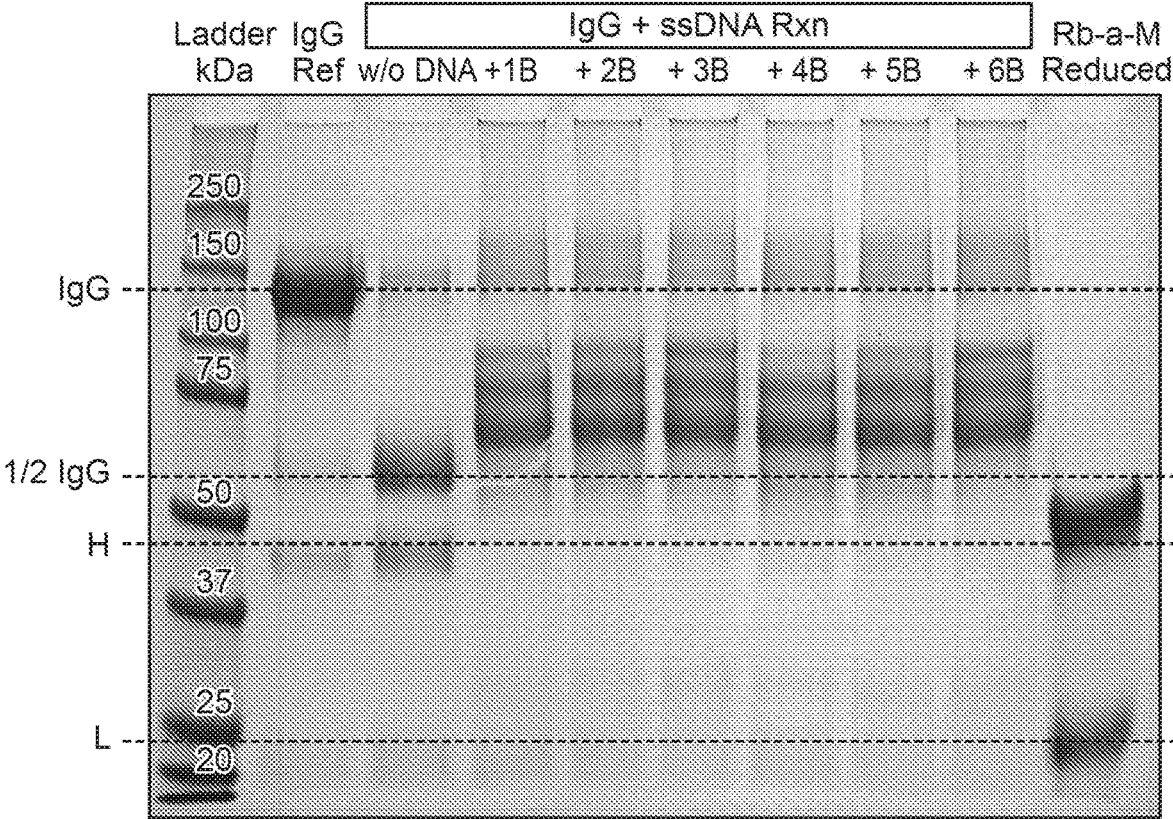


FIG. 8B

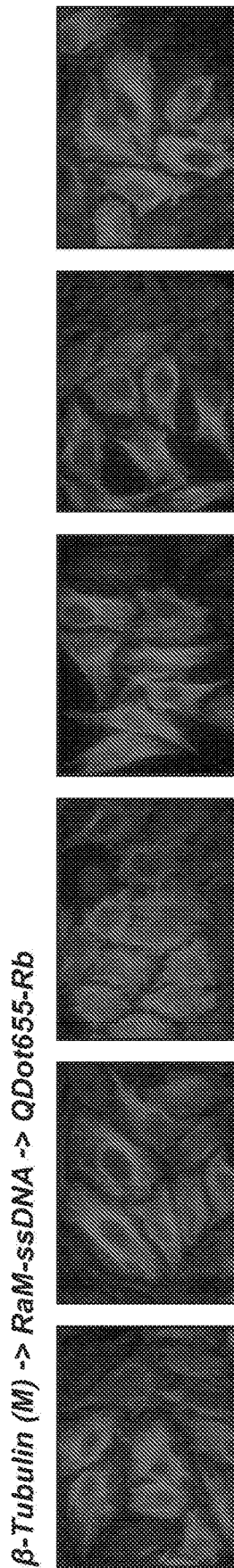


FIG. 9A

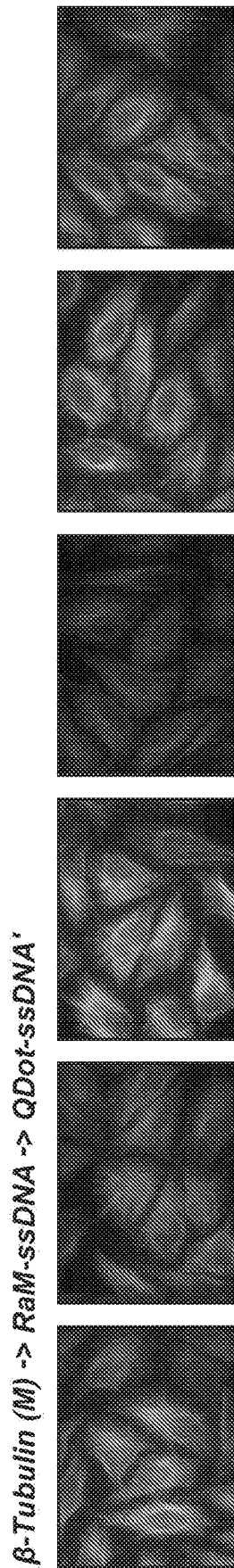


FIG. 9B

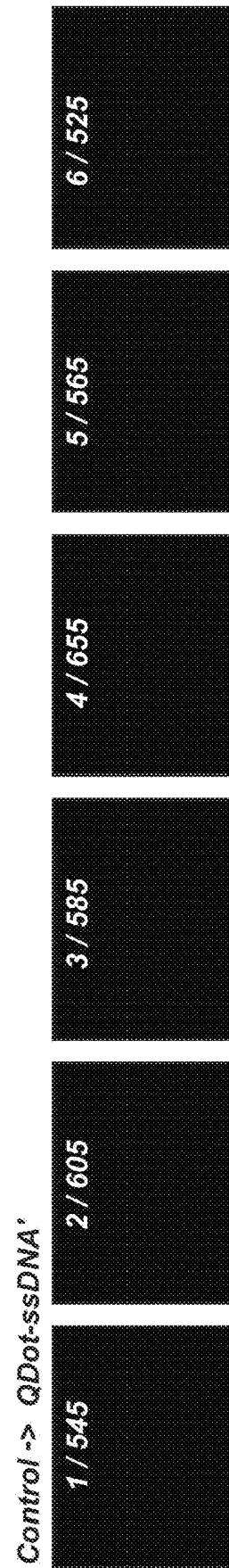


FIG. 9C

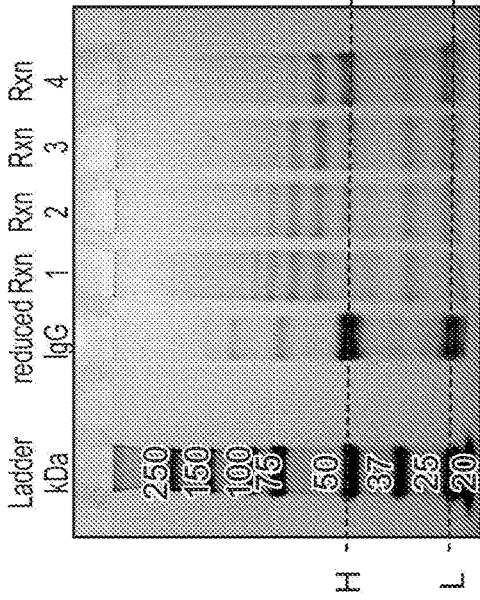
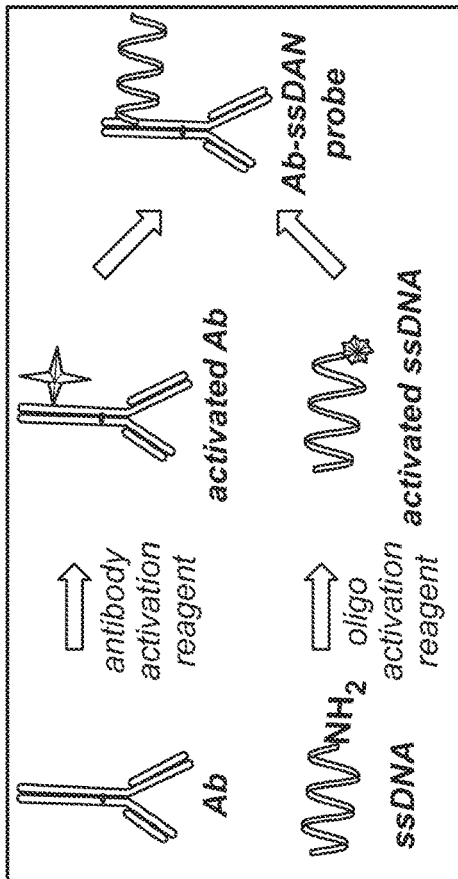


FIG. 10B

FIG. 10A

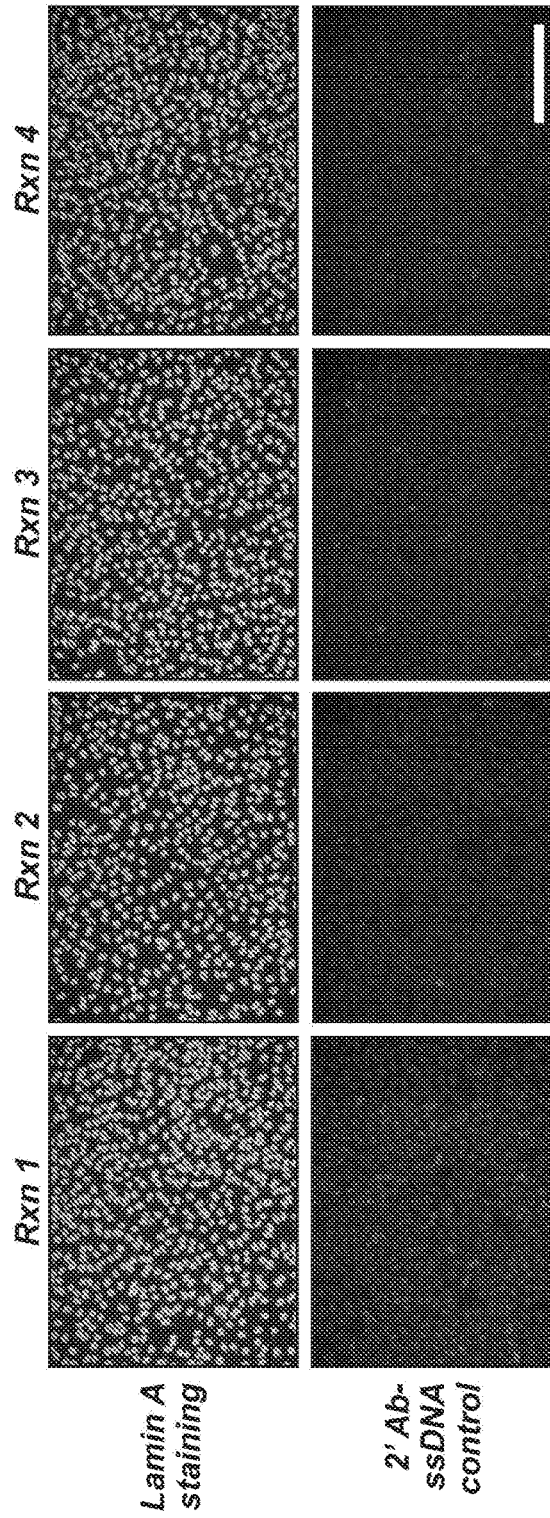


FIG. 10C

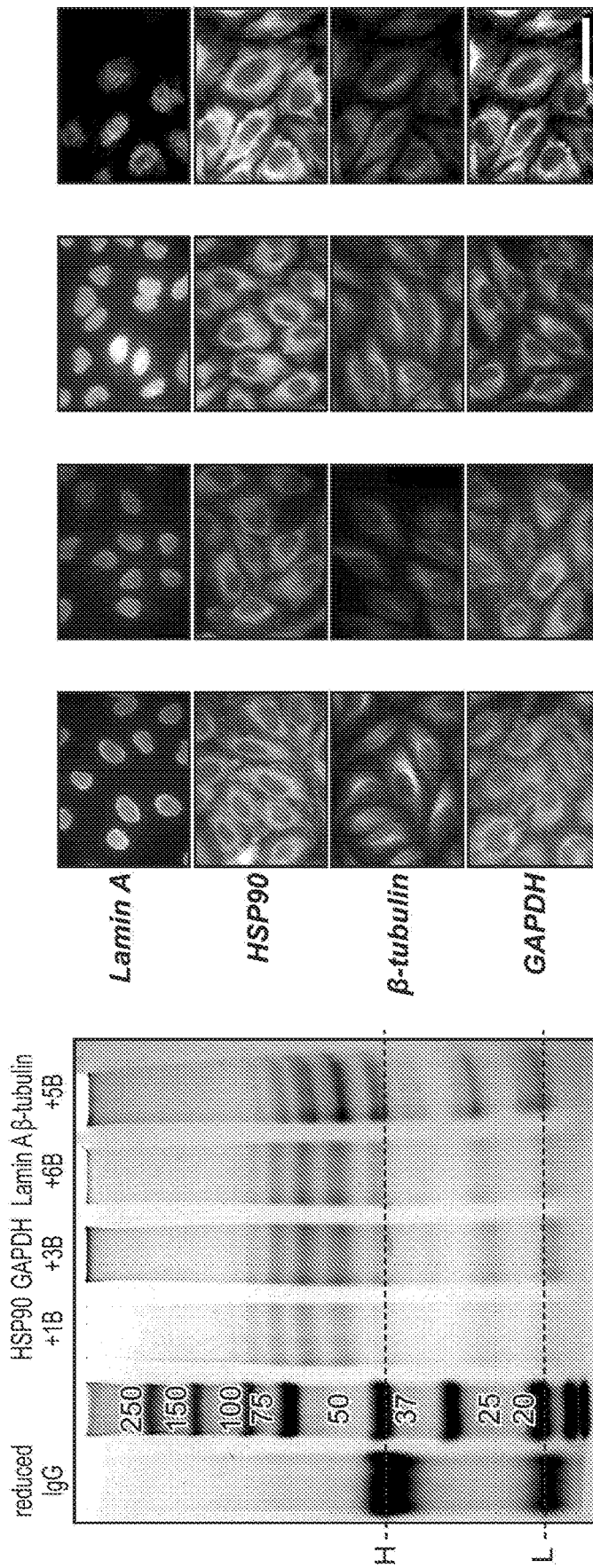


FIG. 11A

FIG. 11B

FIG. 11C

FIG. 11D

FIG. 11E

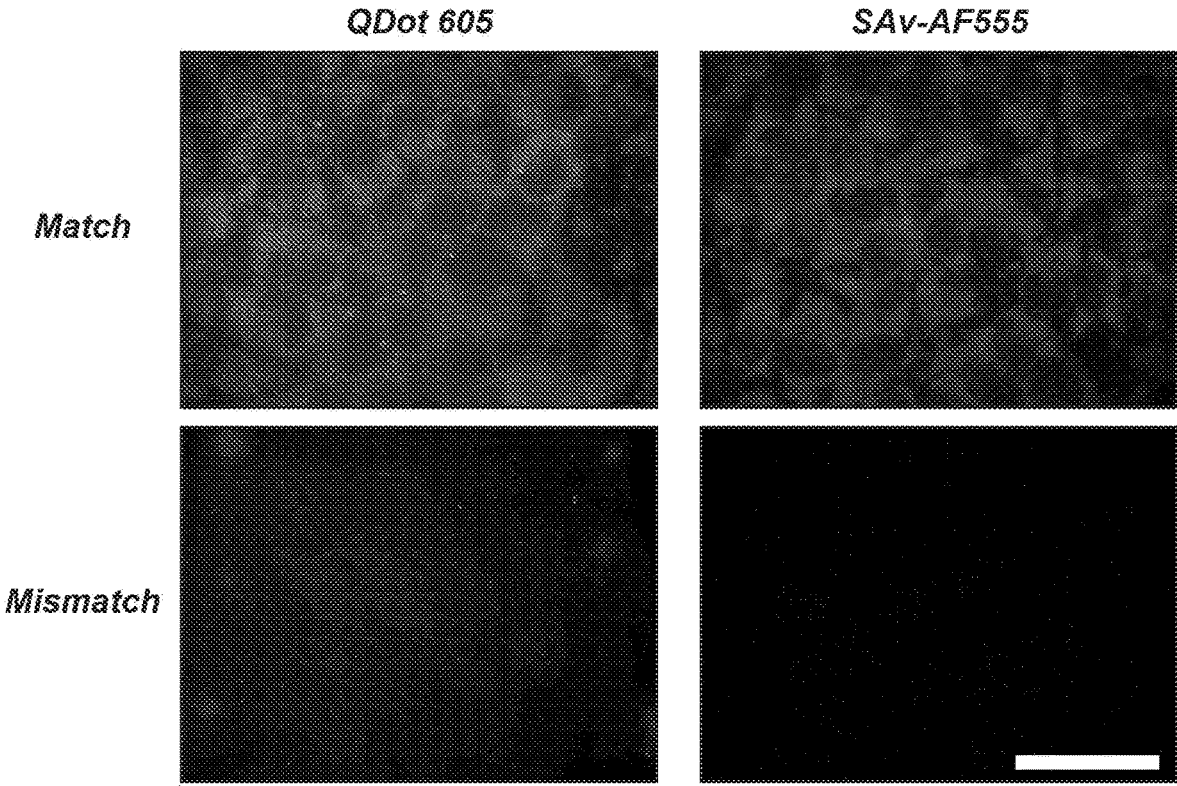


FIG. 12

*HSP90-dsSP-4B*

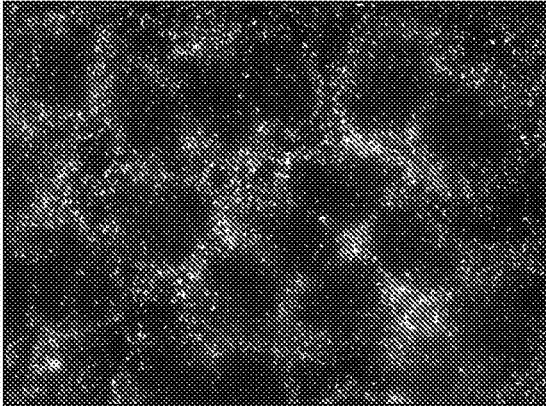


FIG. 13A

*HSP90-4B*

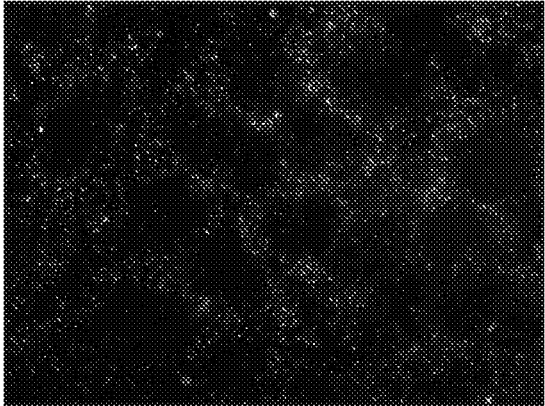


FIG. 13B

*HSP90-ssSP-4B*

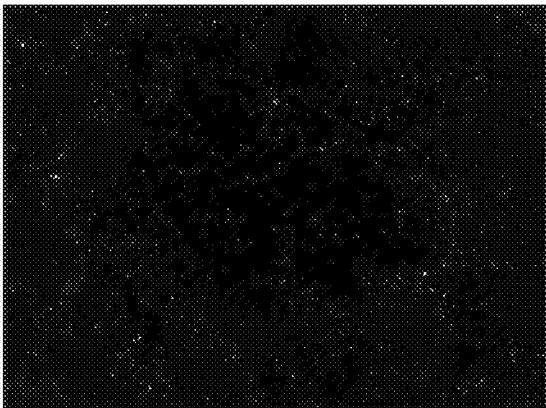


FIG. 13C

*QDot control*

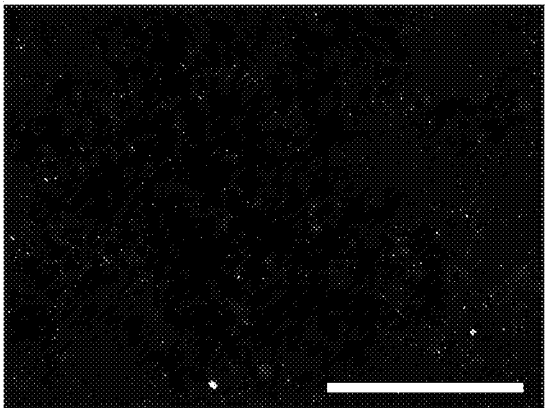


FIG. 13D

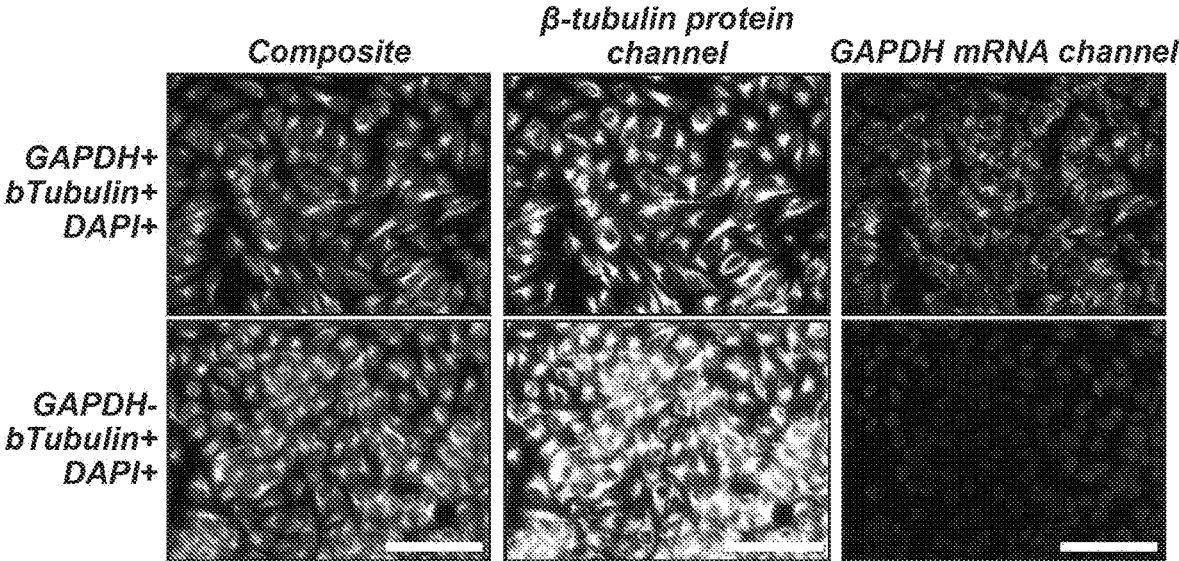


FIG. 14

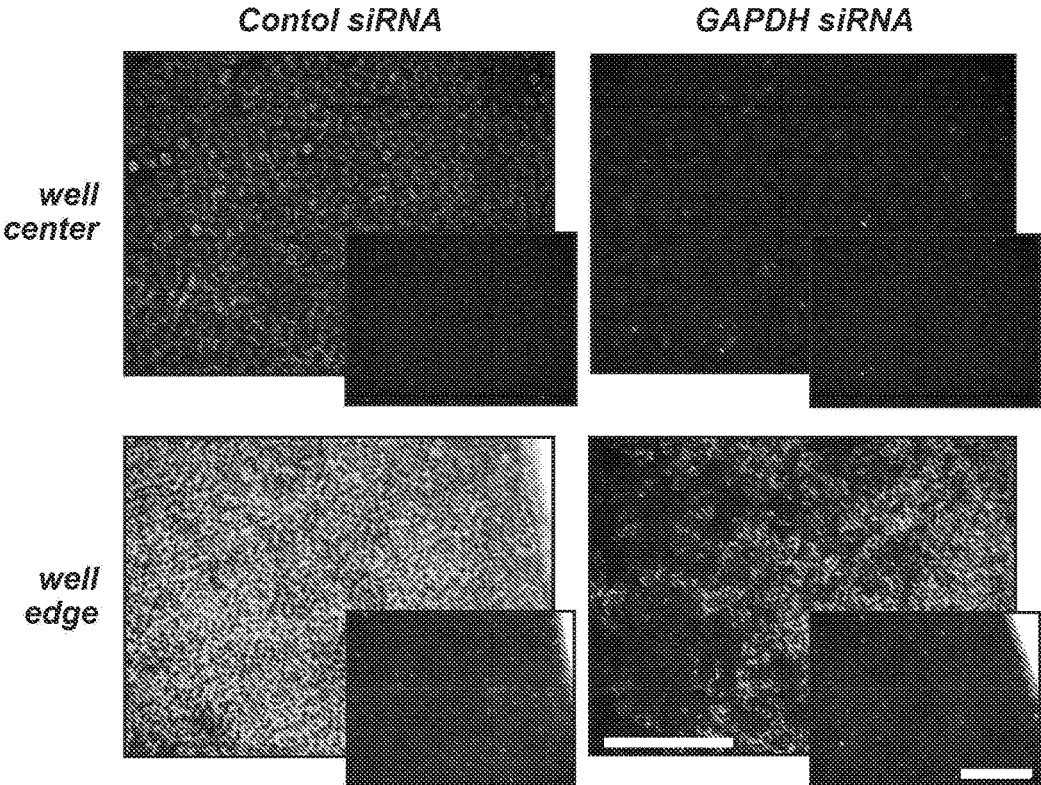


FIG. 15

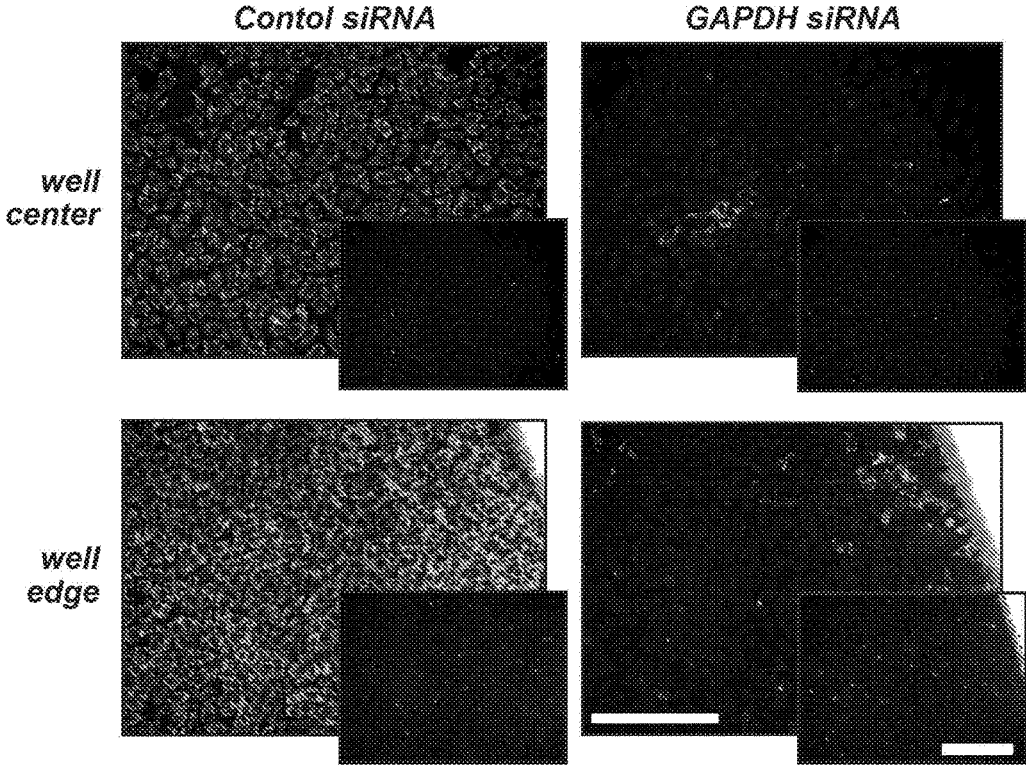


FIG. 16

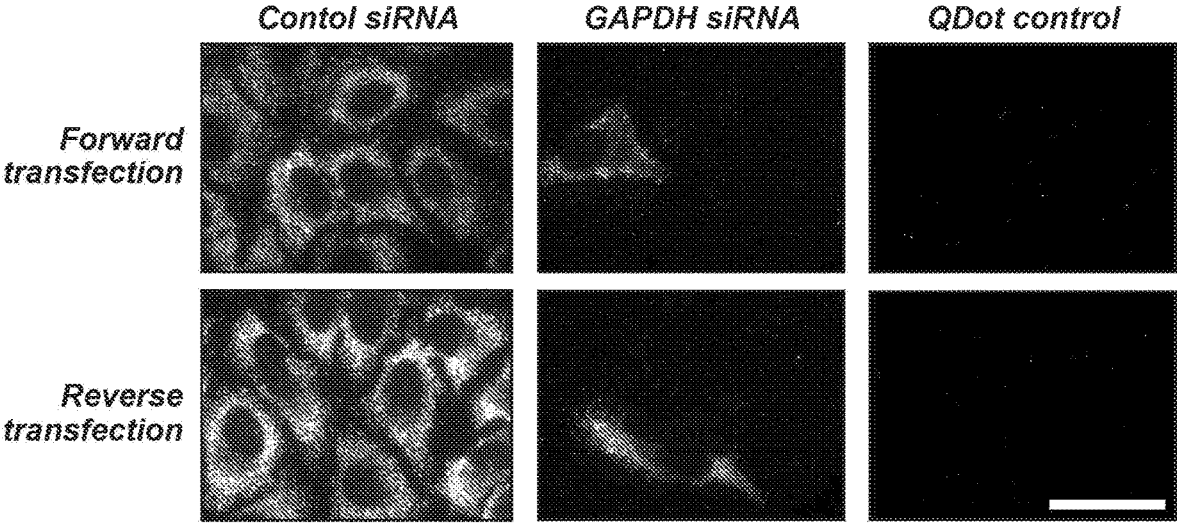
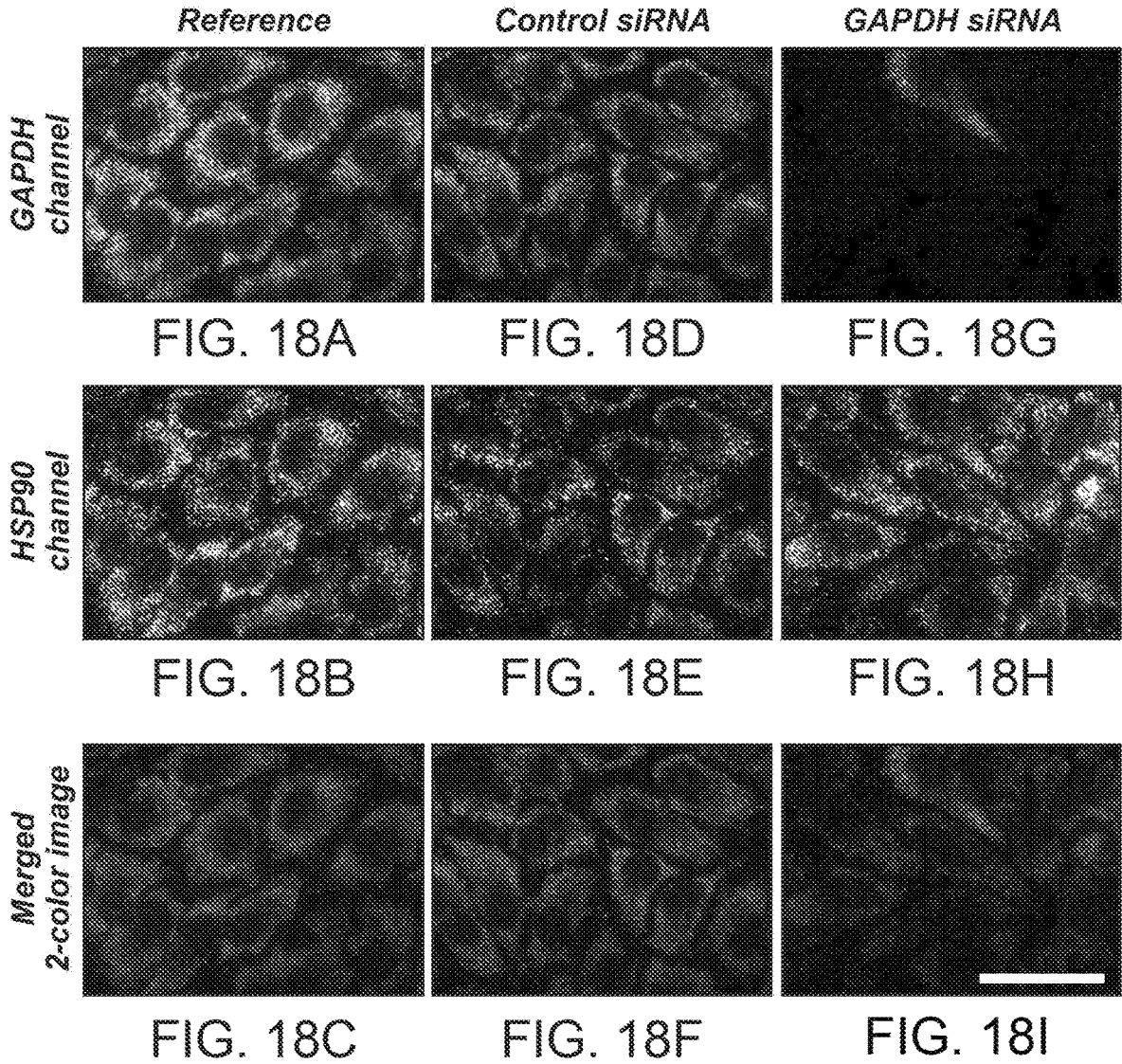


FIG. 17



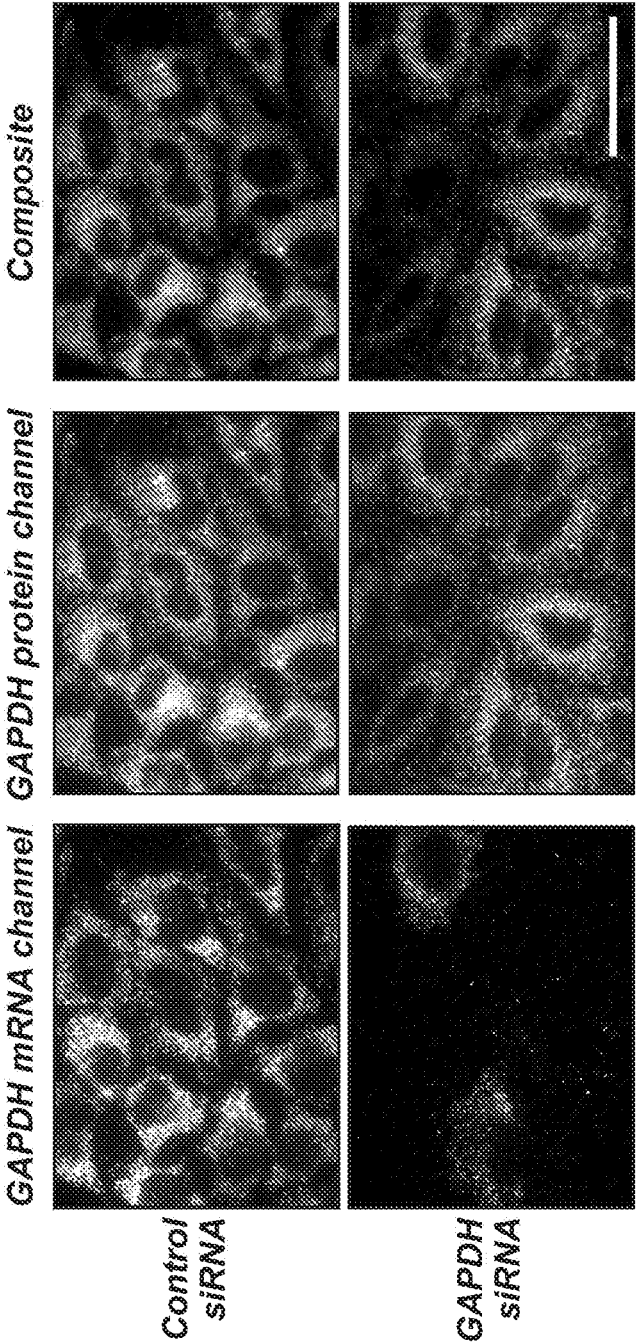


FIG. 19

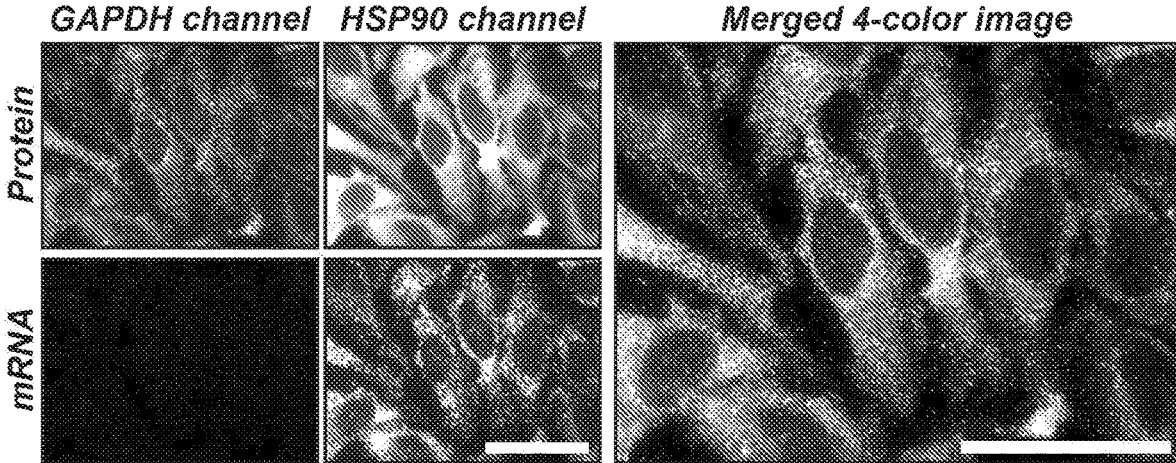


FIG. 20A

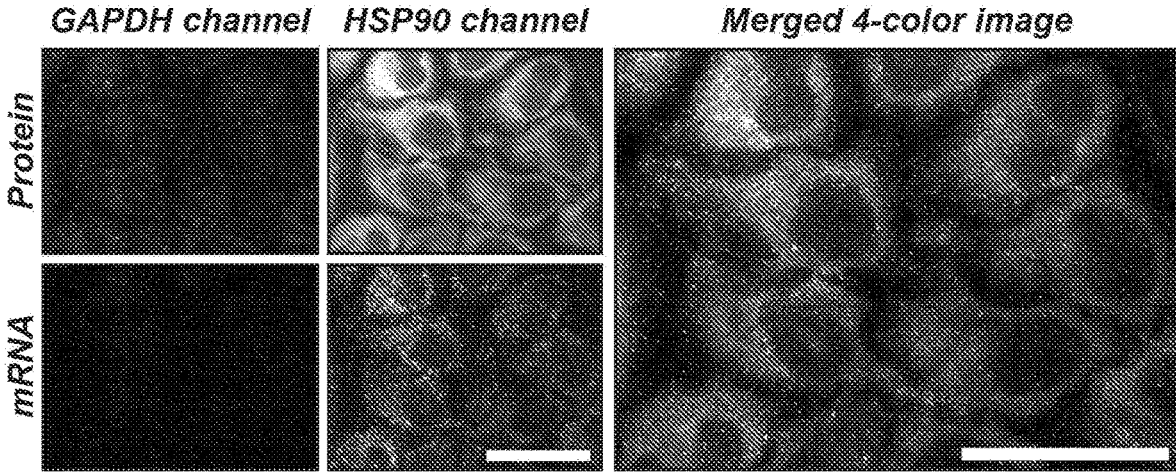


FIG. 20B

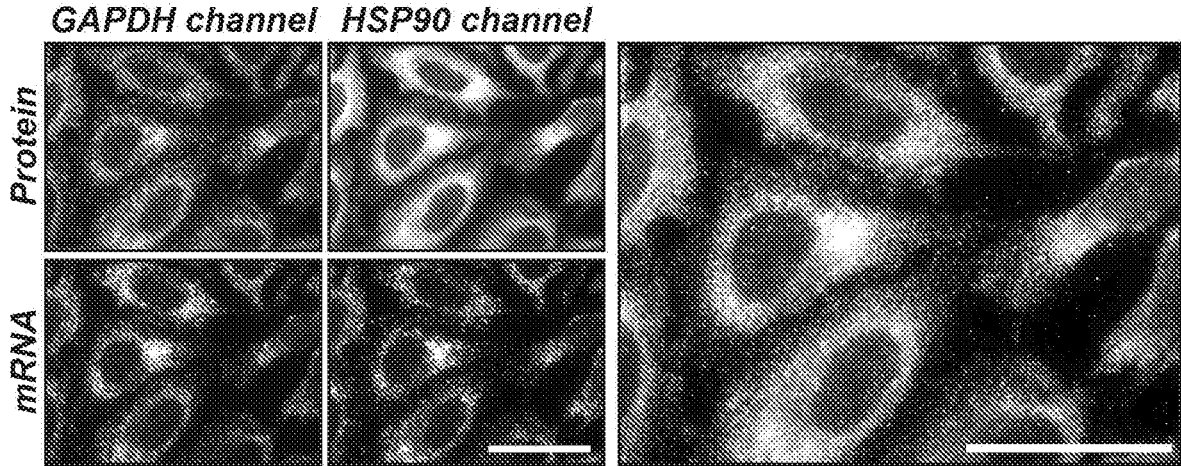


FIG. 21A

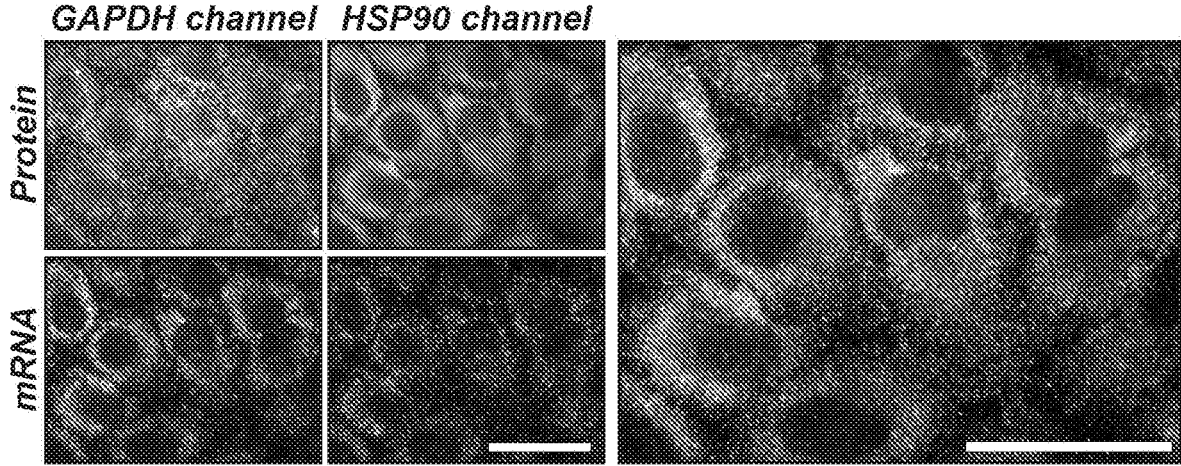


FIG. 21B

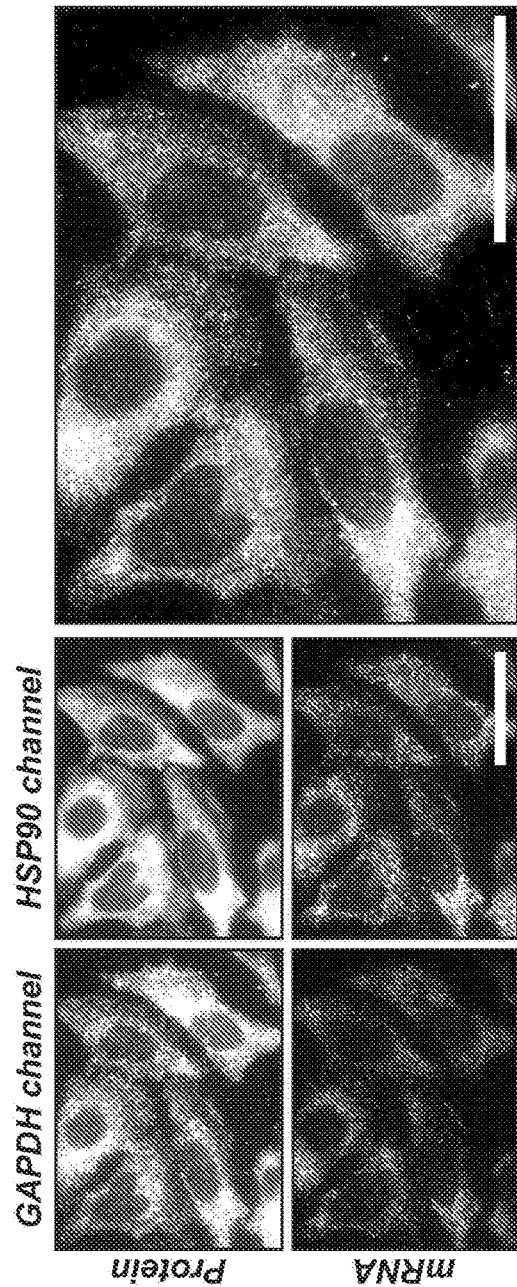


FIG. 22A

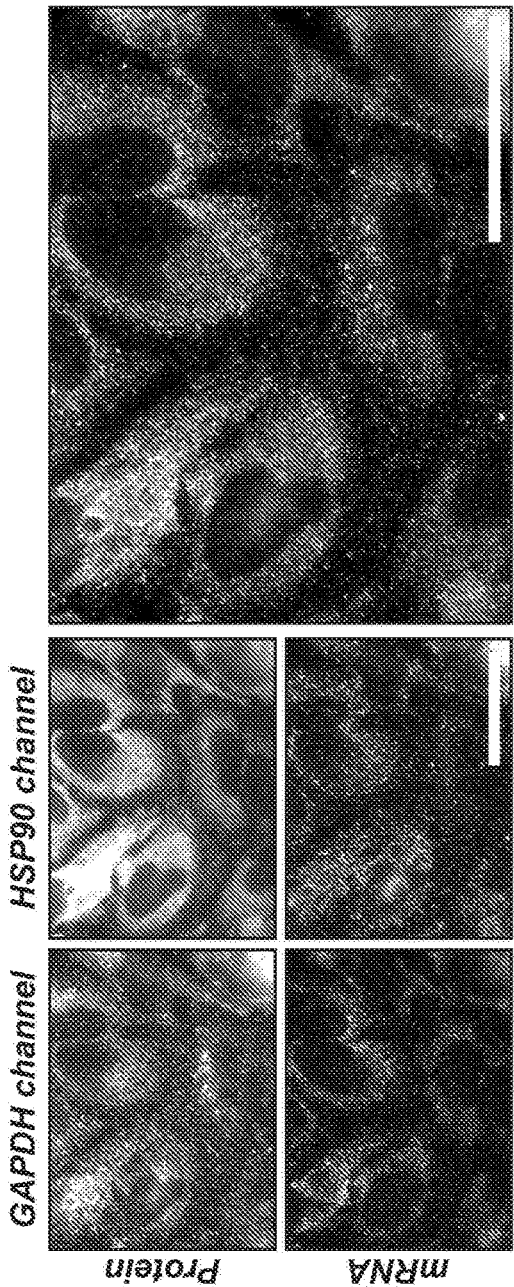


FIG. 22B

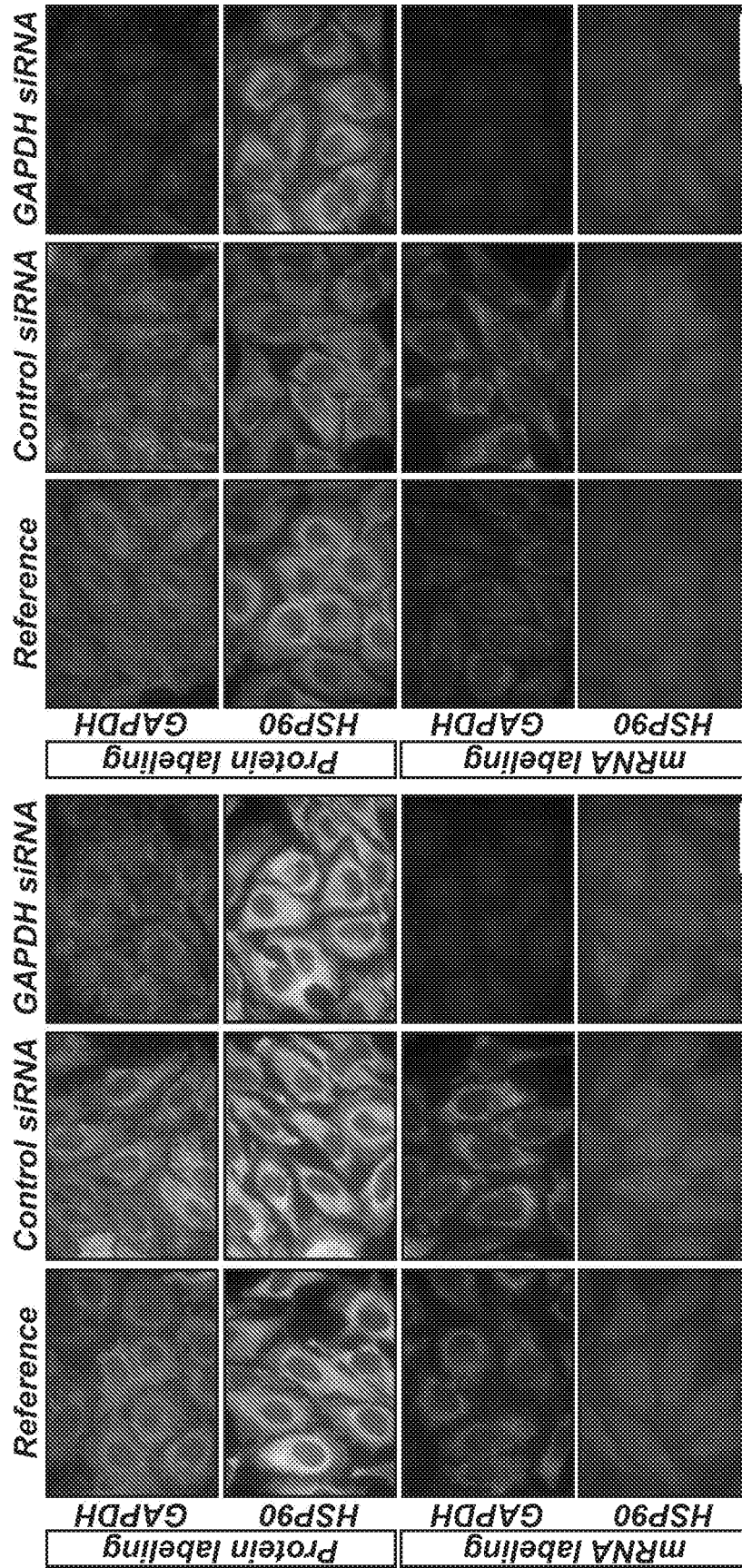


FIG. 23B

FIG. 23A

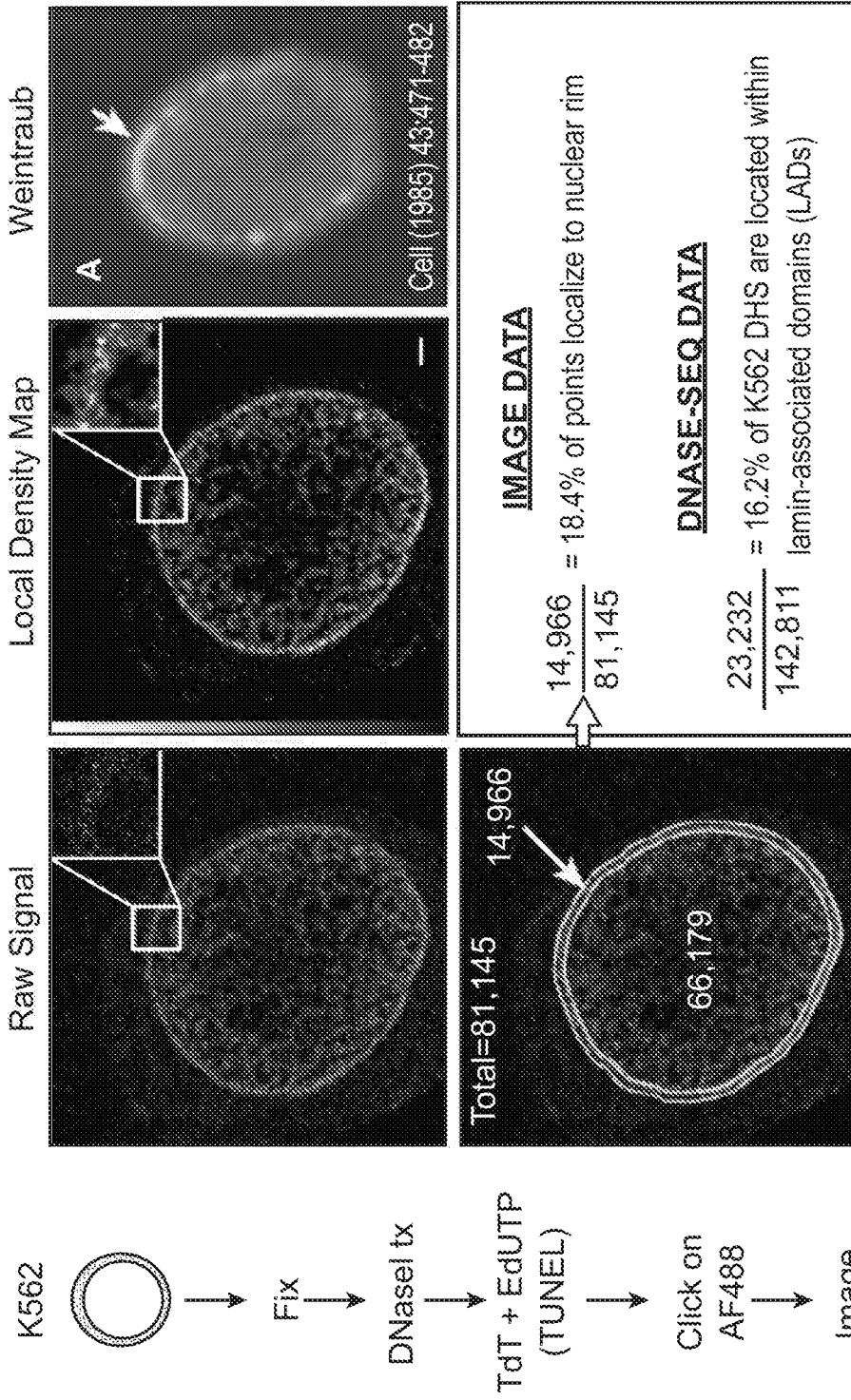


FIG. 24

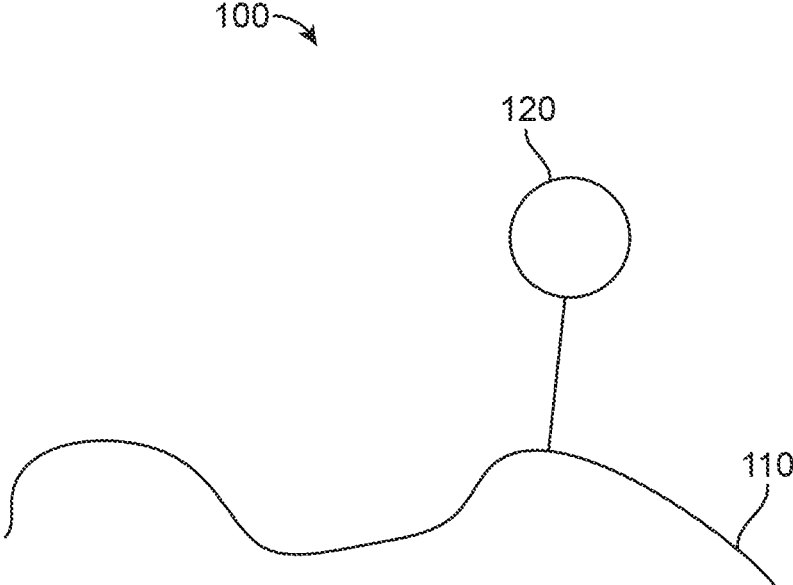


FIG. 25

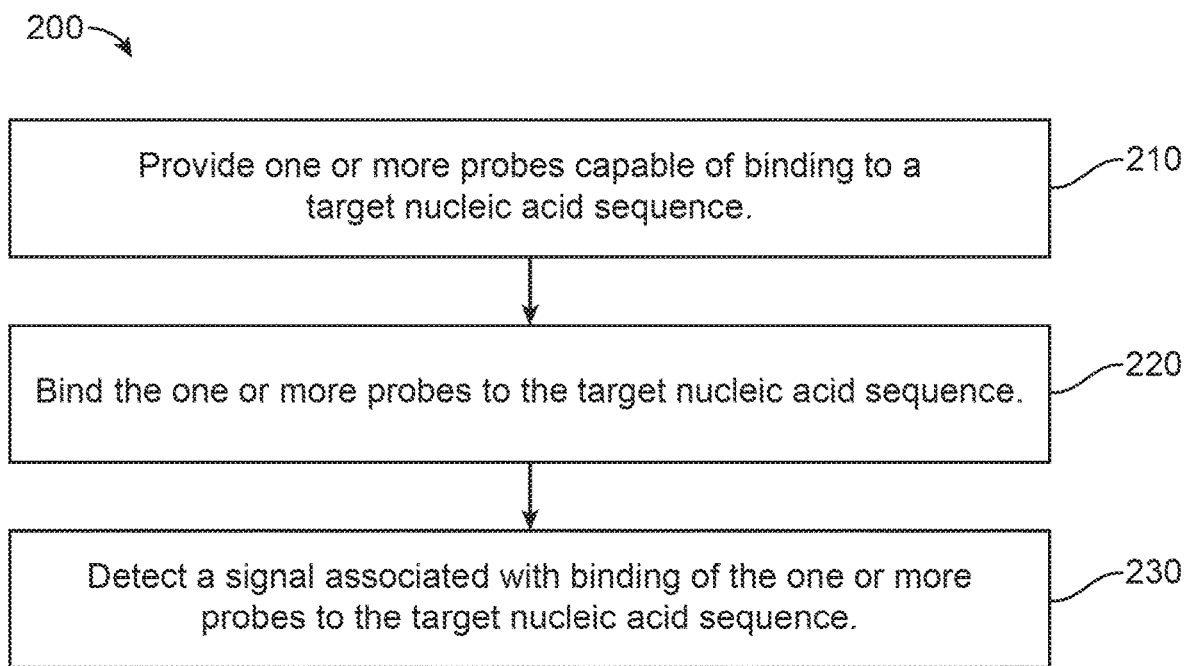


FIG. 26

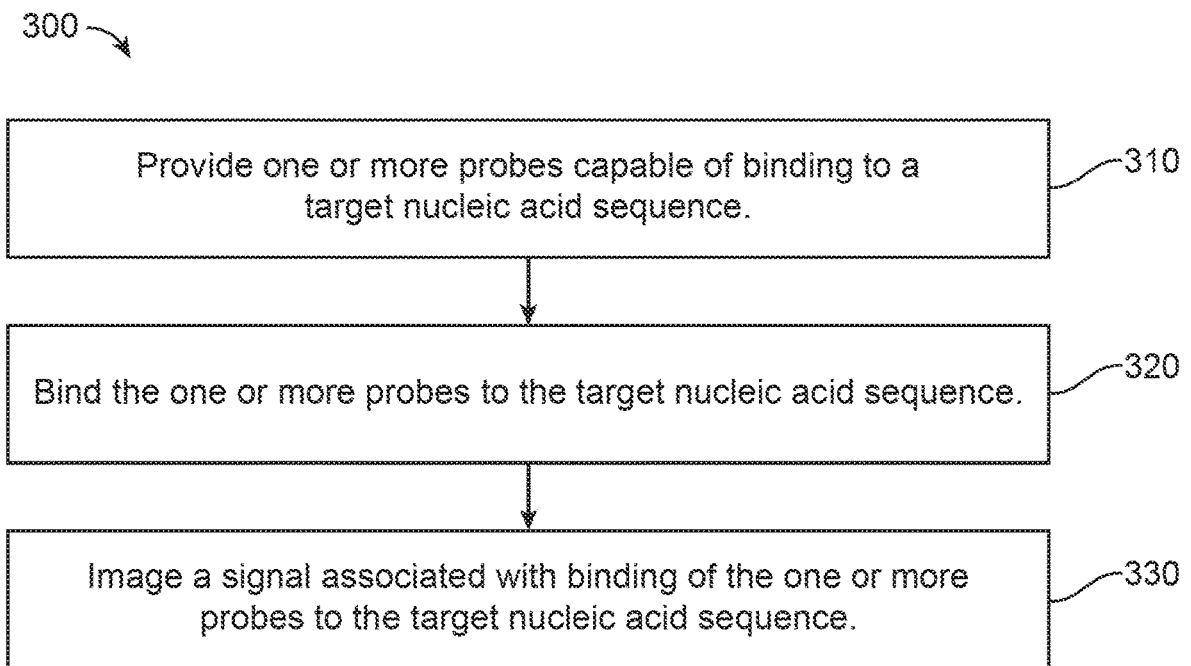


FIG. 27

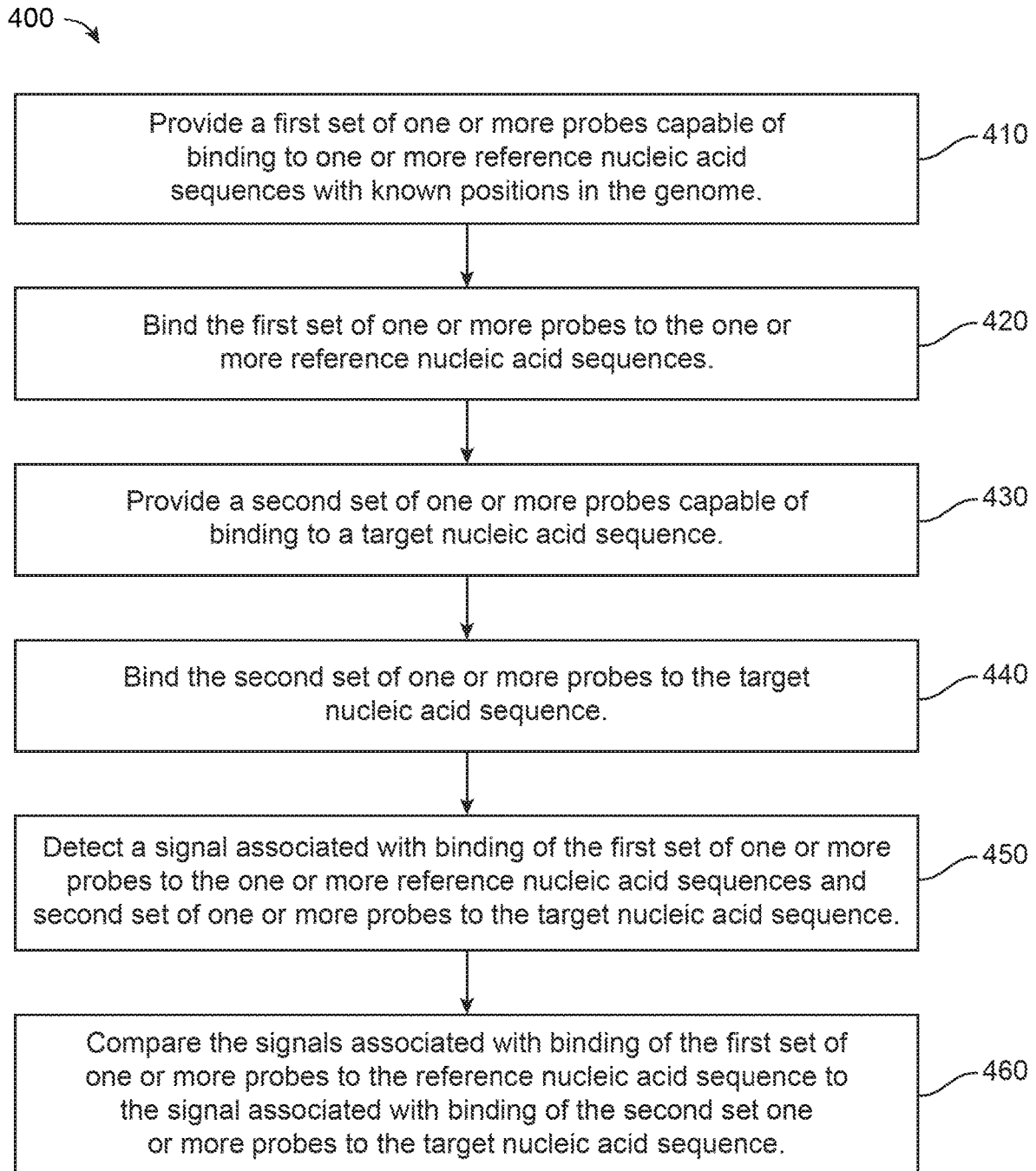


FIG. 28

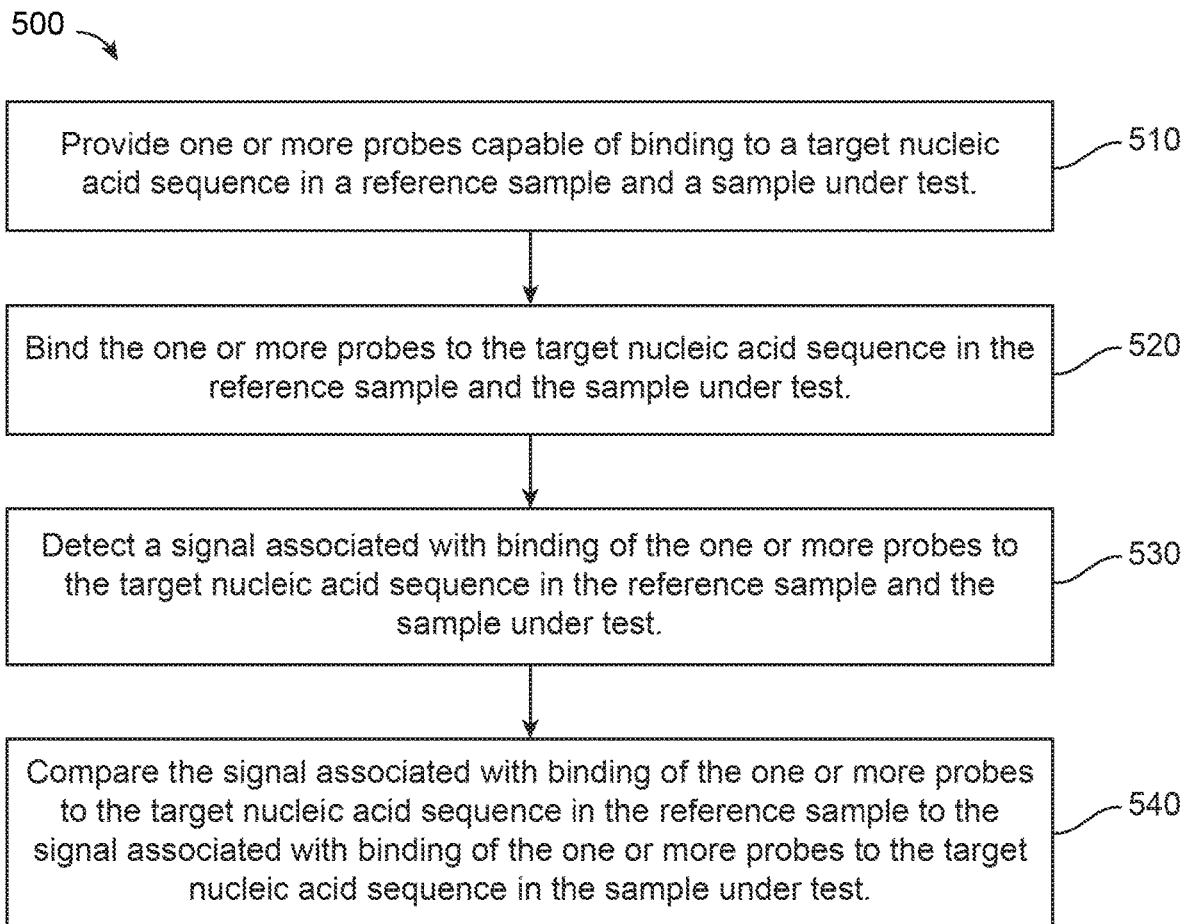


FIG. 29

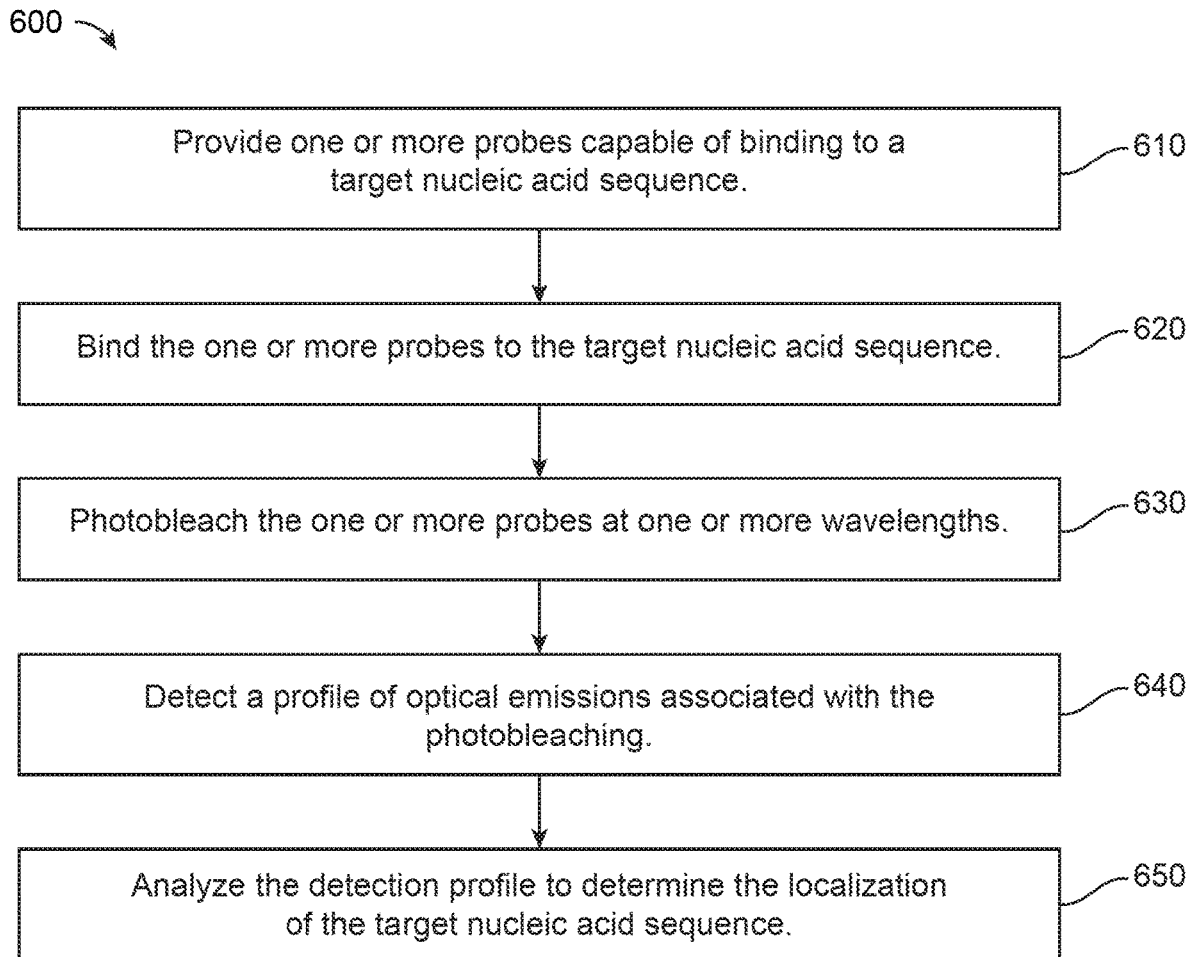


FIG. 30

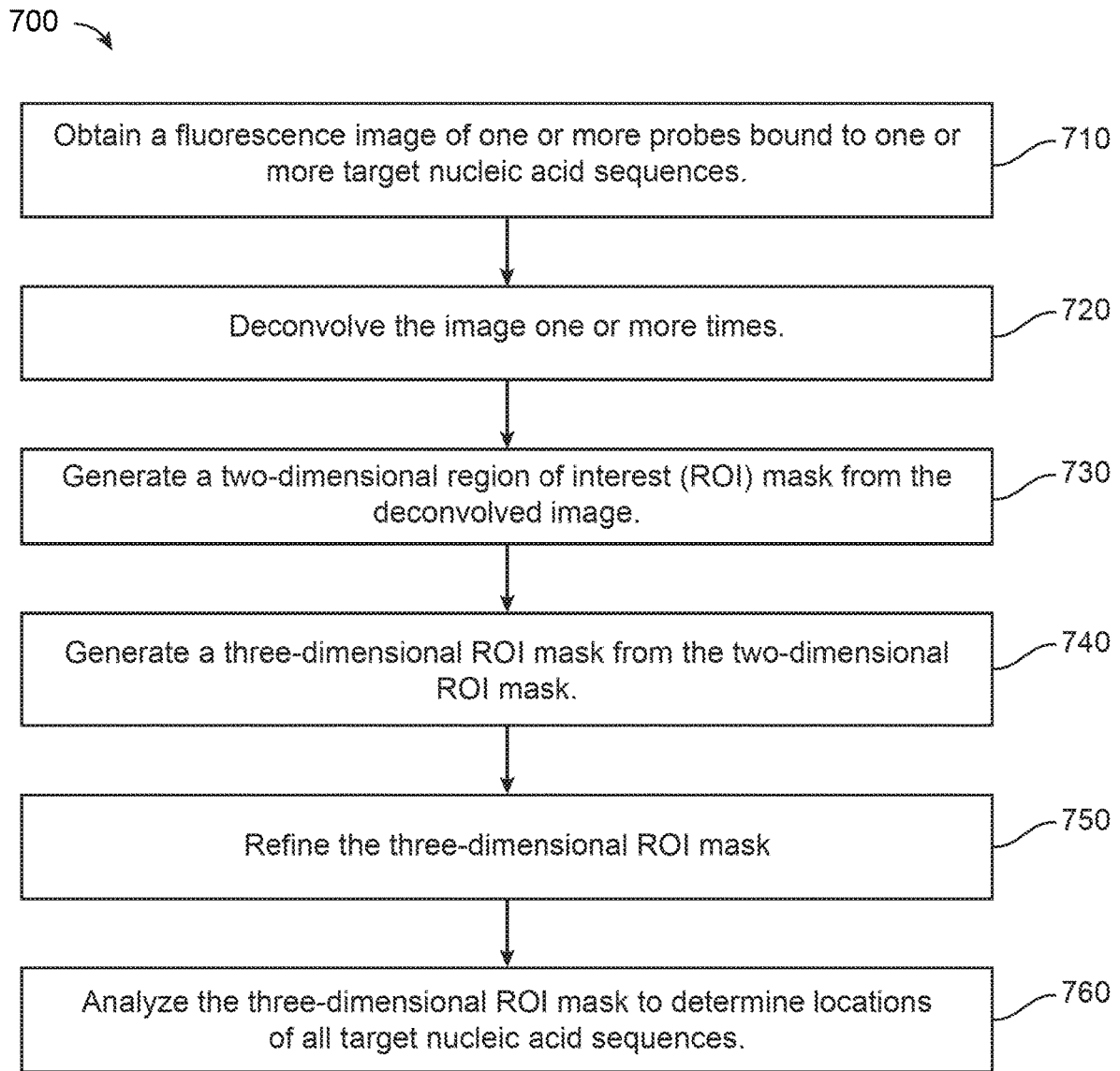


FIG. 31

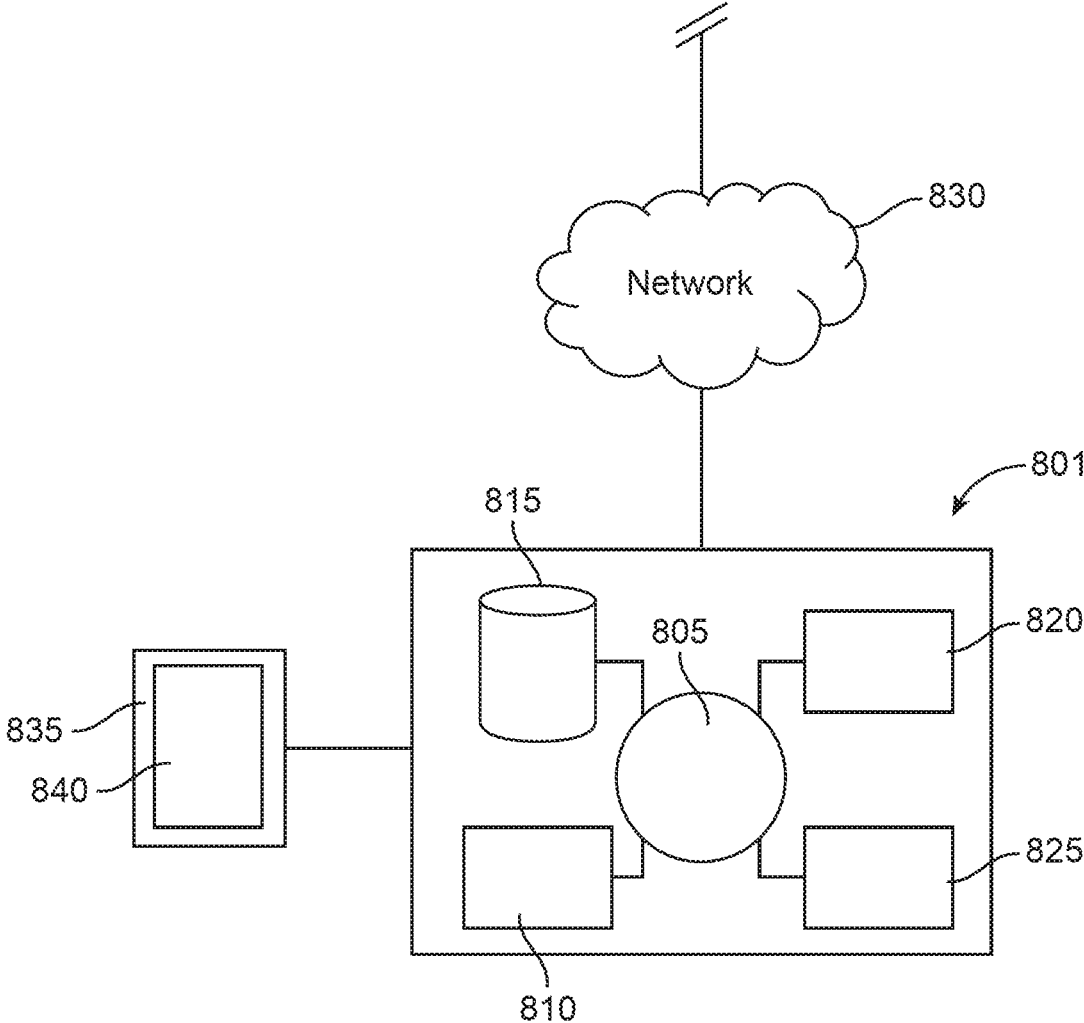


FIG. 32

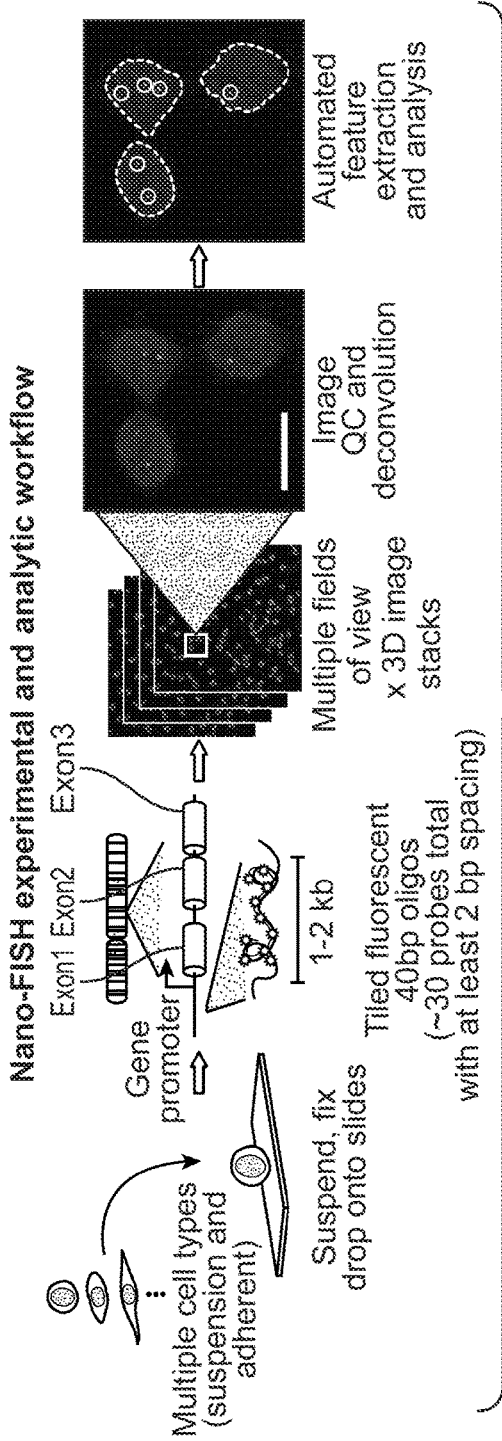


FIG. 33A

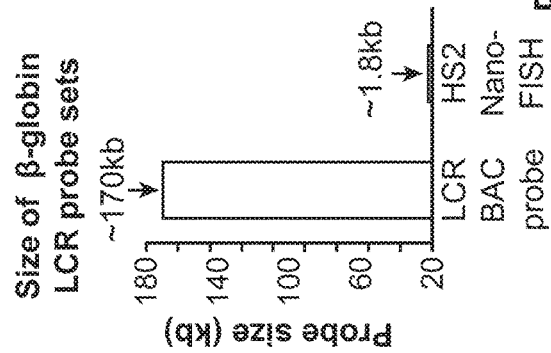


FIG. 33B

Nano-FISH signals co-localize with conventional DNA-FISH probes

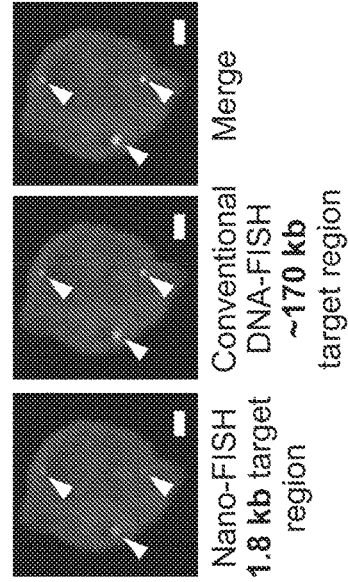


FIG. 33C

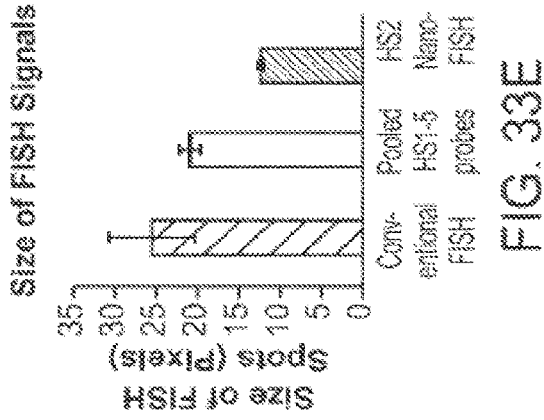


FIG. 33E

Size of target regions for Nano-FISH probe sets

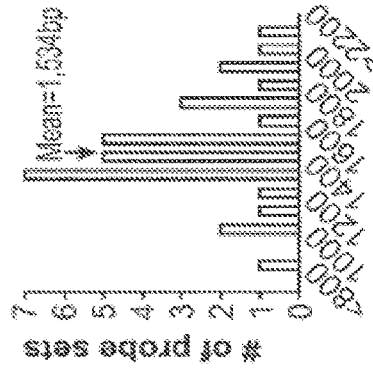


FIG. 33G

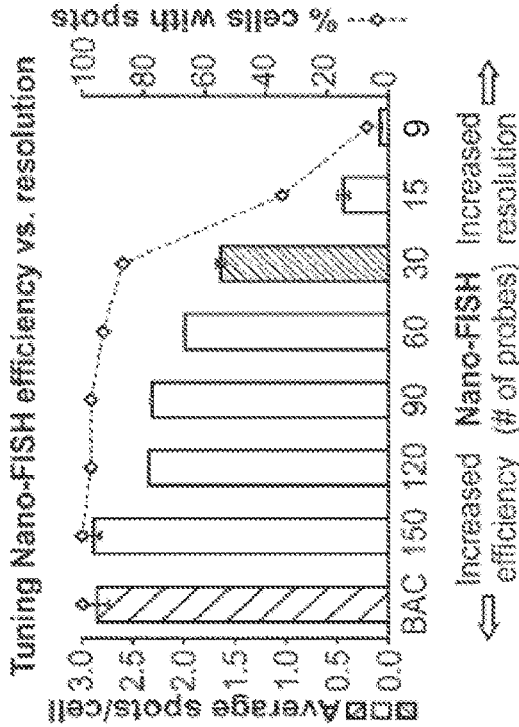


FIG. 33D

Intensity of FISH signals

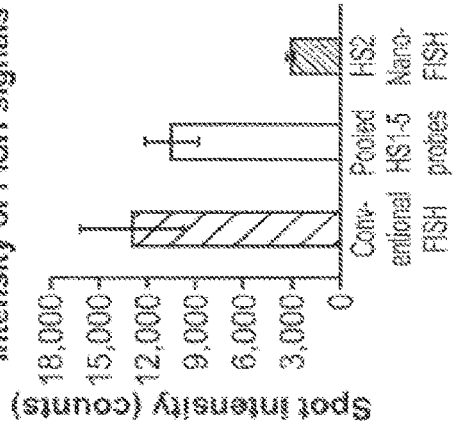


FIG. 33F

Nano-FISH localizes chromosome territories

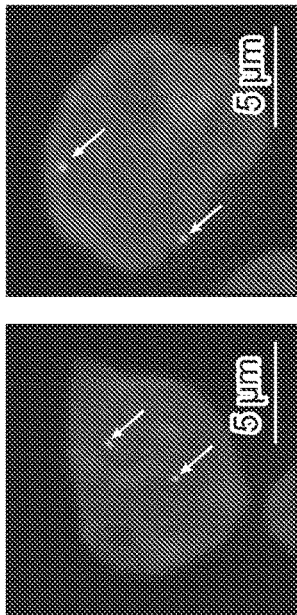
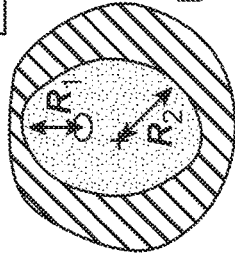
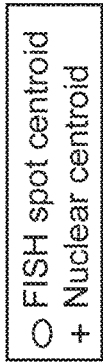


FIG. 34A

Chromosome 19 1.6 kb target region  
 Chromosome 18 1.4 kb target region

Relative radial distance (RRD)



$$RRD = 1 - \frac{R_1}{R_2}$$

FIG. 34B

Positioning of chromosomes

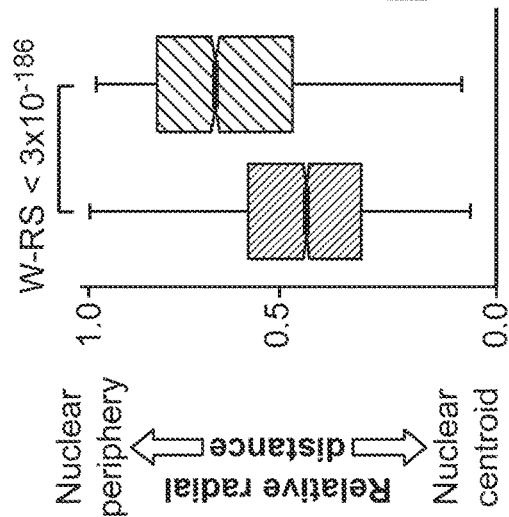


FIG. 34C

Distribution of detected signals relative to the nuclear periphery

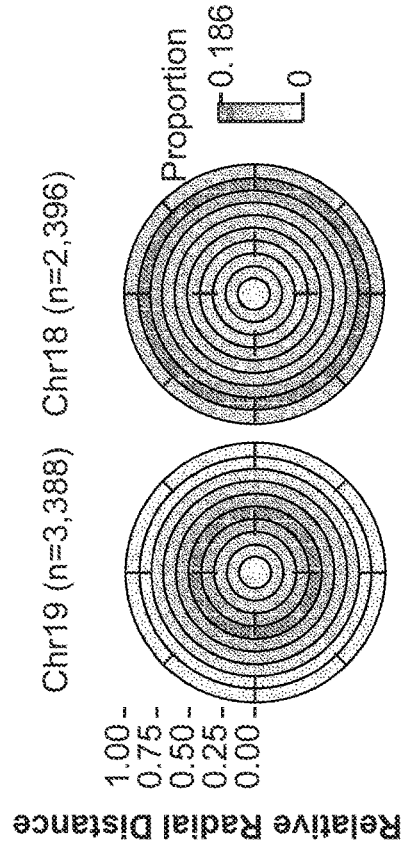


FIG. 34D

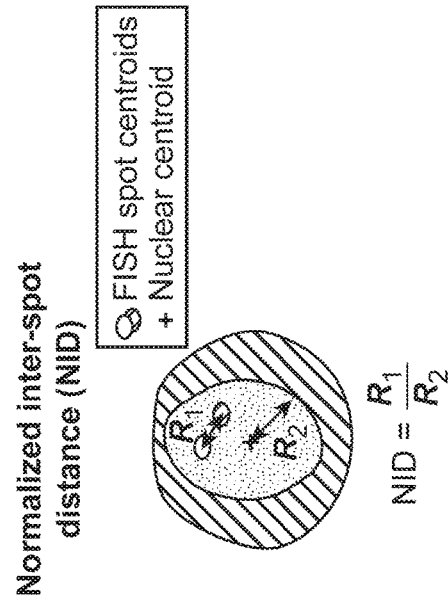
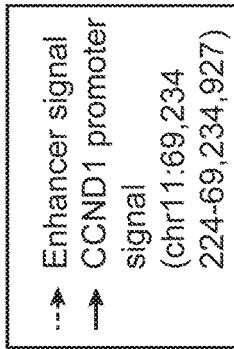
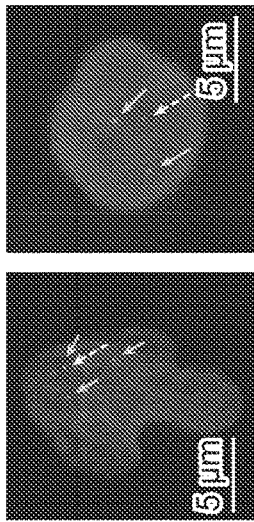


FIG. 35B



Nano-FISH localizes enhancers & promoters



▲ 786-O ACTIVE enhancer — INACTIVE enhancer MCF-7

FIG. 35A

Distance between CCND1 enhancer and promoter

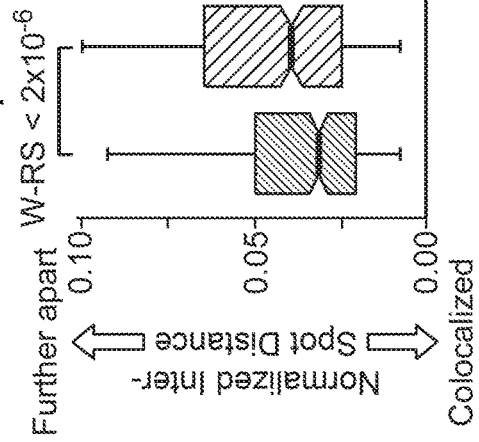


FIG. 35C

Distribution of distances between CCND1 enhancer and promoter

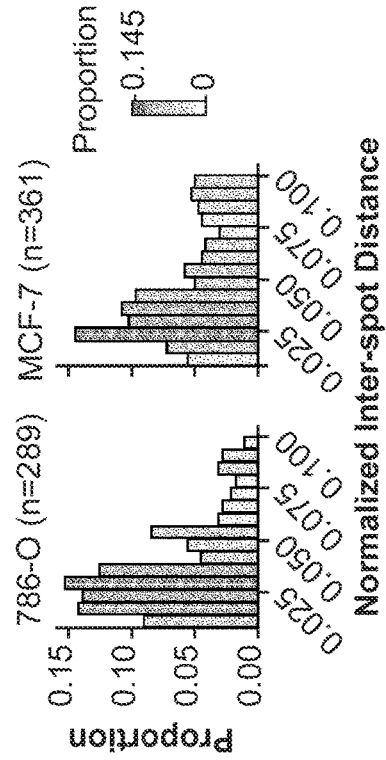


FIG. 35D

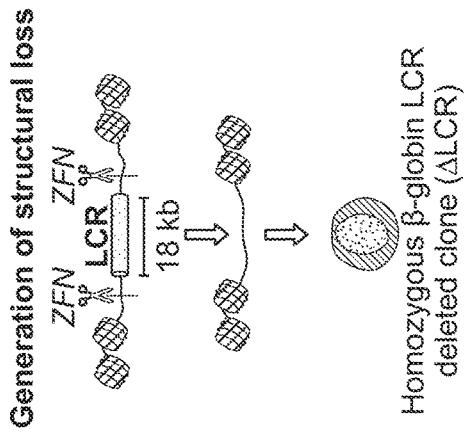


FIG. 36A

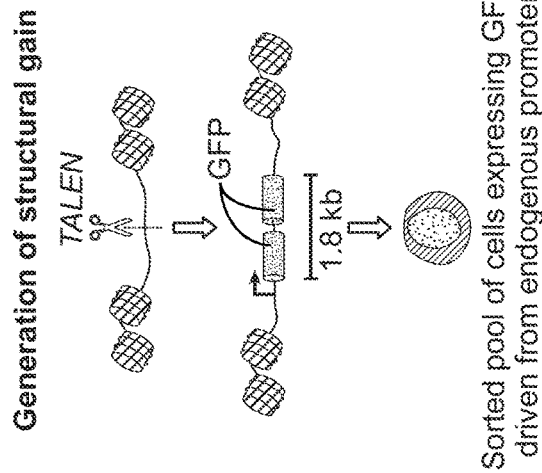


FIG. 36D

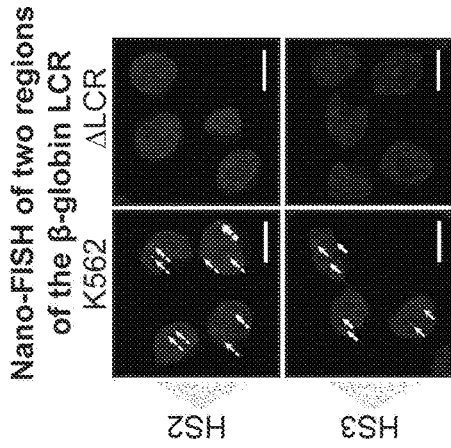


FIG. 36B

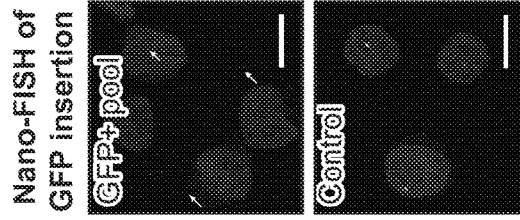


FIG. 36E

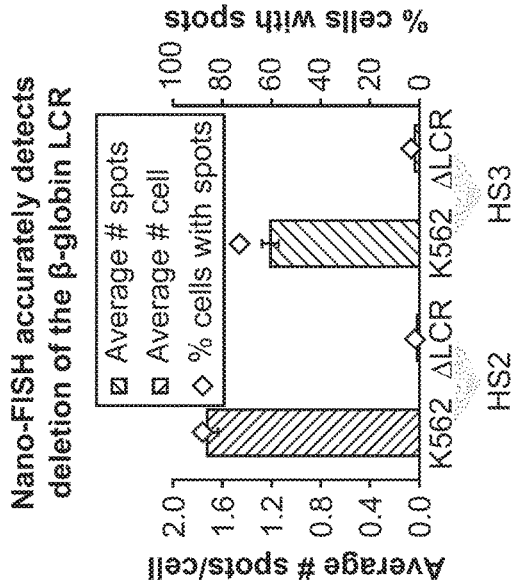


FIG. 36C

**Quantification of GFP insertions by Nano-FISH**

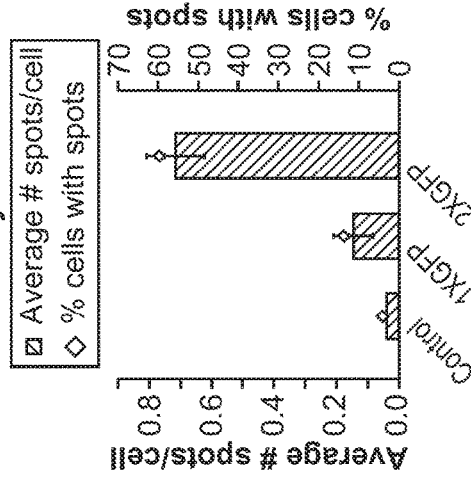
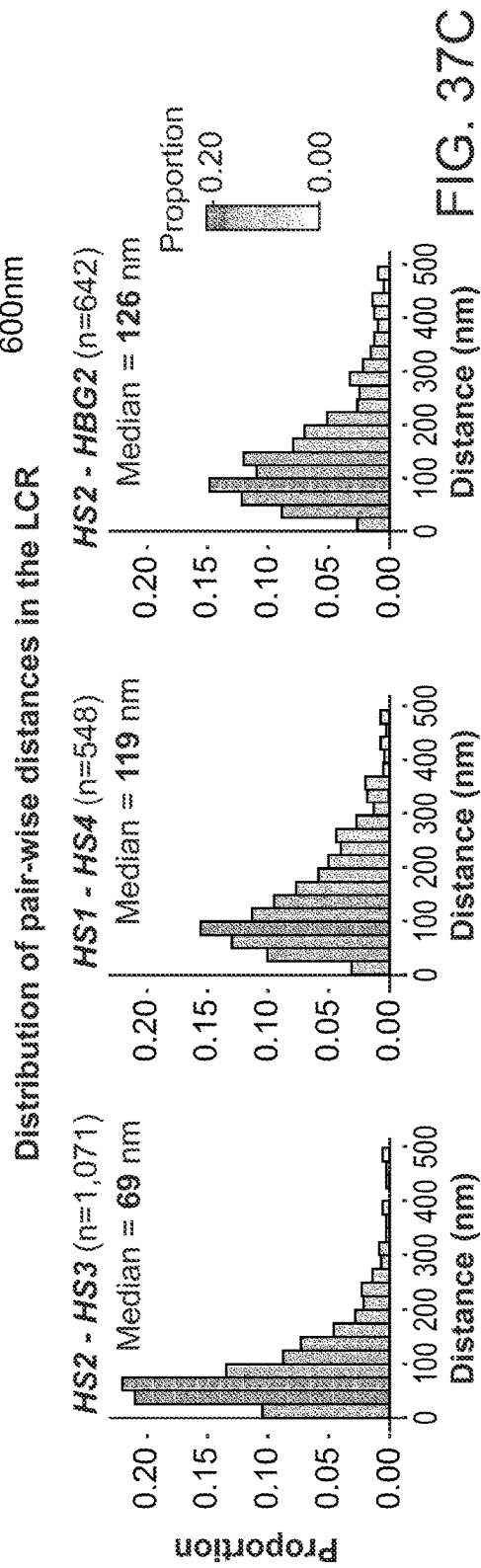
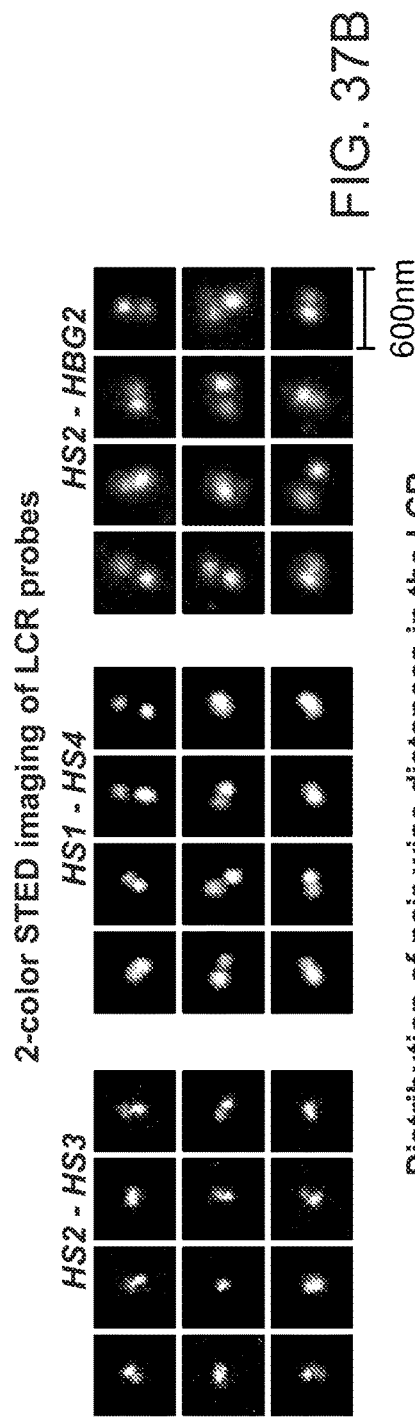
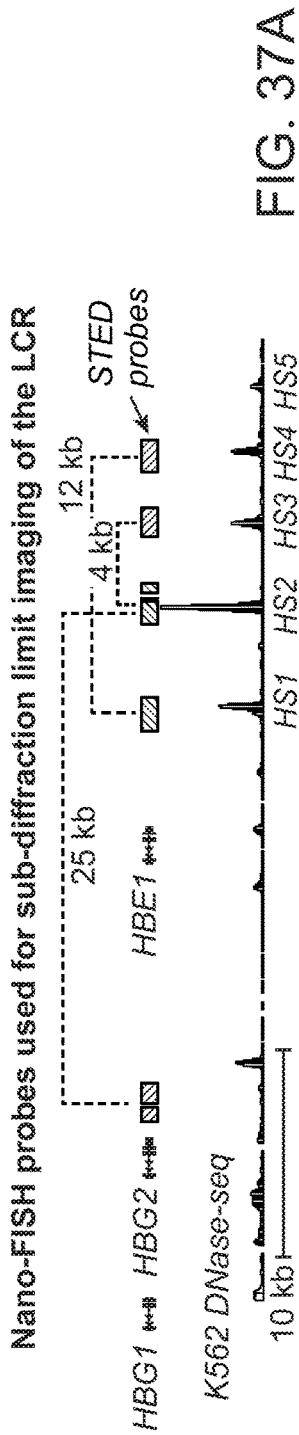


FIG. 36F



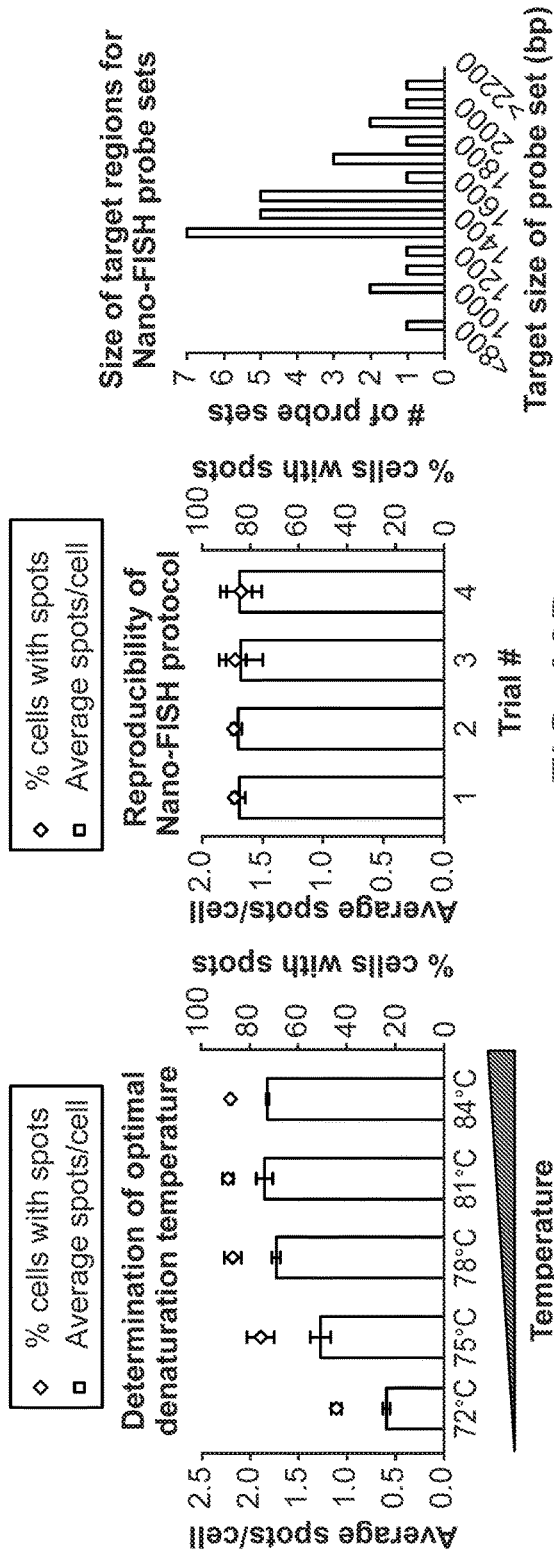


FIG. 38A

FIG. 38B

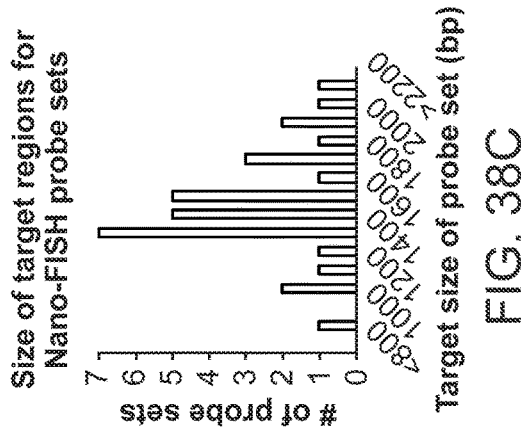


FIG. 38C

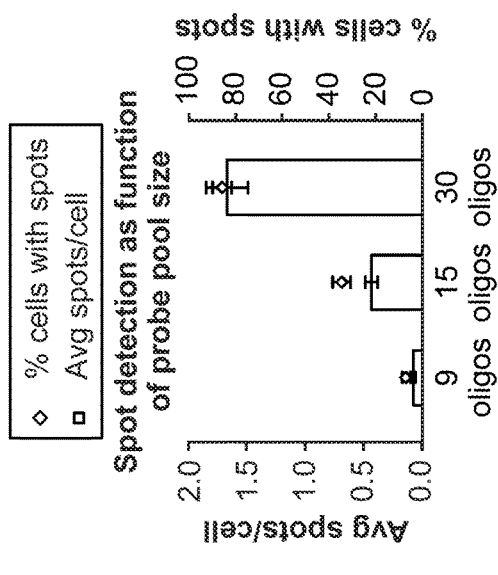


FIG. 38D

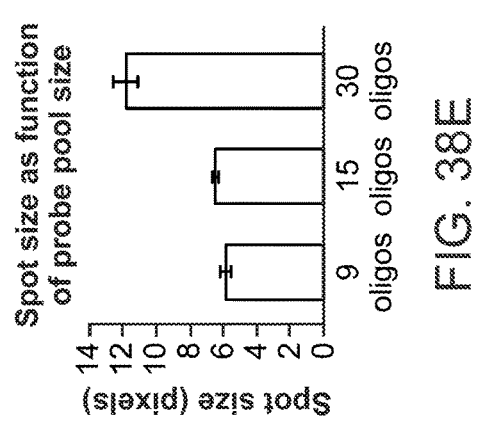


FIG. 38E

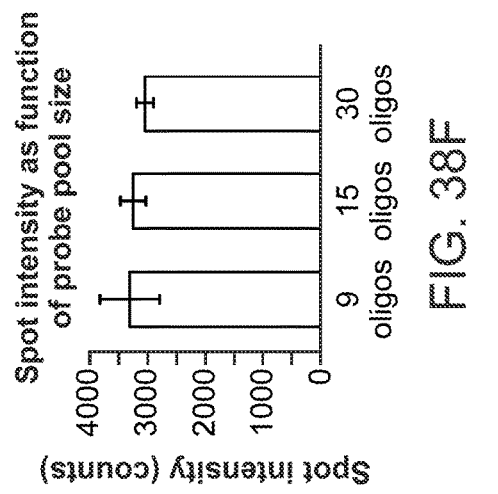


FIG. 38F

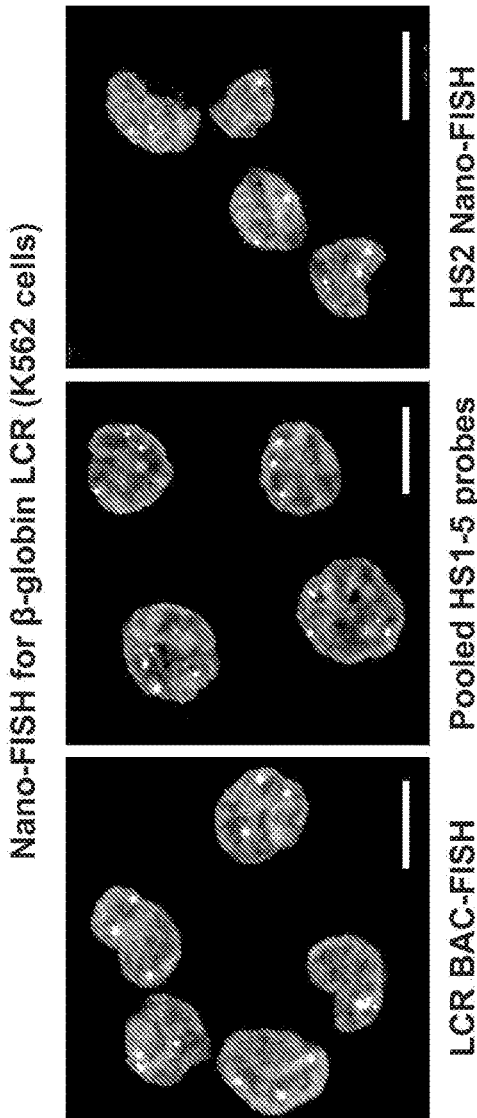


FIG. 39A

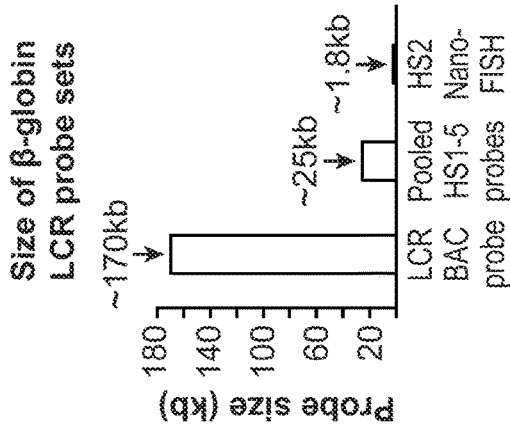


FIG. 39B

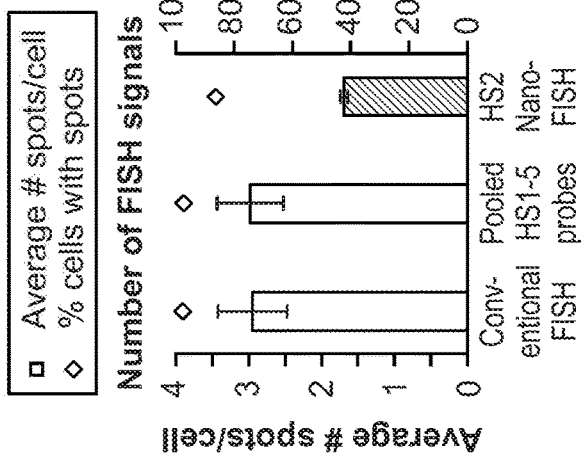


FIG. 39C

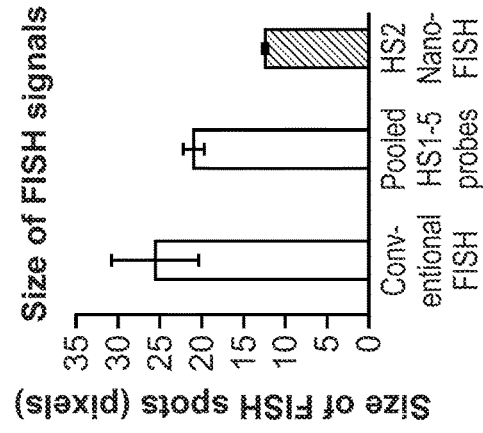


FIG. 39D

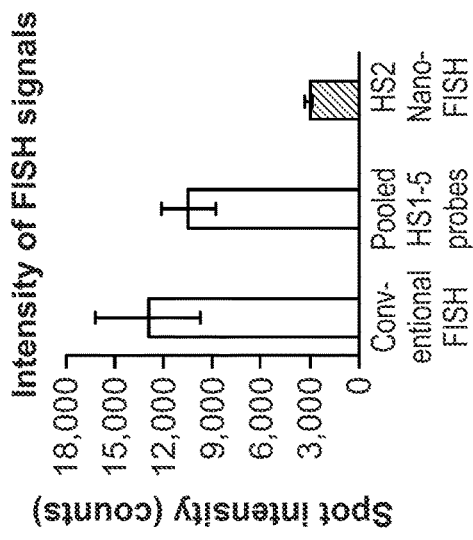


FIG. 39E

## METHODS FOR FLUORESCENCE IMAGING MICROSCOPY AND NANO-FISH

### CROSS-REFERENCE

This application claims the benefit of U.S. Provisional Application No. 62/364,245, filed Jul. 19, 2016, which application is incorporated herein by reference in its entirety for all purposes.

### STATEMENT AS TO FEDERALLY SPONSORED RESEARCH

This invention was made with the support of the United States government under Grant number RM1-HG007743-02 by the Center for Photogenomics.

### BACKGROUND OF THE INVENTION

Imaging techniques such as fluorescence in situ hybridization (FISH) allows for visualization of DNA or RNA regions, and/or assessment of gene expression, chromosome position, and/or protein localization. In some instances, these imaging methods are limited by small field of view and/or limited resolution. As such, data acquisition from large number of cells requires multiple fields of view and thereby presents challenges in obtaining high throughput and high resolution imaging data. Additionally, for example, existing FISH techniques typically use fluorescent probes that span tens to hundreds of kilobases (kb). This precludes the use of existing FISH techniques for accurate detection or spatial localization of smaller genomic sequences. As such, new FISH techniques are required to detect the localization of probes to small genomic sequences.

### SUMMARY OF THE INVENTION

In various aspects, the present disclosure provides a method for detecting a presence of a target nucleic acid sequence in an intact cell, the method comprising: a) providing a nucleic acid sequence comprising the target nucleic acid sequence in the intact cell, wherein the target nucleic acid sequence is less than 2.5 kilobases in length; b) contacting the intact cell with a first plurality of probes, wherein each probe comprises a first detectable label and a probe sequence that binds to a portion of the target nucleic acid sequence; and c) detecting a presence of the first detectable label in the intact cell, wherein the presence of the first detectable label indicates the presence of the target nucleic acid sequence. In some aspects, the detecting is within a period of not more than 48 hours.

In various aspects, a method comprises detecting a target nucleic acid sequence within a period of not more than 48 hours, wherein the target nucleic acid sequence is a non-amplified target nucleic acid sequence. In further aspects, the method comprises contacting the target nucleic acid sequence with a first plurality of probes, wherein each probe comprises a first detectable label and probe sequence that binds to a portion of the target nucleic acid sequence. In still further aspects, the method comprises detecting a presence of the first detectable label on the target nucleic acid sequence, wherein the presence of the first detectable label indicates the presence of the target nucleic acid sequence.

In various aspects, a method for quantifying a target nucleic acid sequence in an intact cell is provided herein, the method comprising: a) providing a nucleic acid sequence comprising the target nucleic acid sequence in the intact cell;

b) contacting the intact cell with a first plurality of probes, wherein each probe comprises a first detectable label and a probe sequence that binds to a portion of the target nucleic acid sequence; and c) determining a number of the target nucleic acid sequences present in the intact cell within a period of not more than 48 hours.

In some aspects, the target nucleic acid sequence comprises a nucleic acid sequence of not more than 10 kilobases in length, not more than 8 kilobases in length, not more than 6 kilobases in length, not more than 4 kilobases in length, not more than 3 kilobases in length, not more than 2 kilobases in length, not more than 1.5 kilobases in length, or not more than 1 kilobases in length.

In some aspects, the method further comprises: d) contacting the intact cell with a second detectable label that binds to a portion of a cellular structure, and e) detecting a position of the first detectable label in the intact cell relative to the second detectable label, wherein the position is used to determine a spatial position of the target nucleic acid sequence.

In other aspects, the method further comprises: d) providing the intact cell further comprising a second target nucleic acid sequence; e) contacting the intact cell with a second plurality of probes, wherein each probe comprises a second detectable label and a probe sequence that binds to a portion of the second target nucleic acid sequence, and f) detecting a position of the first detectable label in the intact cell relative to the second detectable label, wherein the position is used to determine the spatial position of the target nucleic acid sequence.

In some aspects, the target nucleic acid sequence comprises an exogenous nucleic acid sequence. In some aspects, the target nucleic acid sequence comprises a nucleic acid sequence encoding somatic rearrangement. In some aspects, the target nucleic acid sequence comprises a nucleic acid sequence encoding a B cell receptor or a T cell receptor.

In some aspects, the method comprises the first plurality of probes bound to the nucleic acid sequence is less than 250 probes, less than 200 probes, less than 150 probes, less than 100 probes, less than 80 probes, less than 60 probes, less than 50 probes, less than 40 probes, less than 30 probes, less than 20 probes, less than 15 probes, less than 10 probes, or less than 8 probes.

In some aspects, the period is not more than 24 hours.

In some aspects, the method further comprises binding at least a portion of the first plurality of probes to the target nucleic acid sequence.

In some aspects, the method further comprises washing the intact cell after contacting the target nucleic acid sequence with the first plurality of probes. In some aspects, the method further comprises optically detecting the first detectable label. In some aspects, the method further comprises optically detecting the second detectable label.

In some aspects, the intact cell is obtained from a tissue. In some aspects, the intact cell is a mammalian or eukaryotic cell. In some aspects, the intact cell is a hematopoietic progenitor cell, a monocyte, a macrophage, a microglia, a neuron, or a T-cell.

In some aspects, the method further comprises introducing the exogenous nucleic acid sequence into the cell. In some aspects, the introducing comprises electroporation, lipofection, transfection, microinjection, viral transduction, or use of a gene gun. In some aspects, the exogenous nucleic acid sequence is integrated into the genome of the cell.

In some aspects, the probe sequence of at least one probe of the first plurality of probes comprises an oligonucleotide sequence. In some aspects, the probe sequence of at least one

probe of the first plurality of probes comprises an amino acid sequence. In some aspects, the second plurality of probes bound to the second target nucleic acid sequence is less than 250 probes, less than 200 probes, less than 150 probes, less than 100 probes, less than 80 probes, less than 60 probes, less than 50 probes, less than 40 probes, less than 30 probes, less than 20 probes, less than 15 probes, less than 10 probes, or less than 8 probes. In some aspects, the probe sequence of at least one probe of the second plurality of probes comprises an oligonucleotide sequence. In some aspects, the probe sequence of at least one probe of the second plurality of probes comprises an amino acid sequence.

In various aspects, the present disclosure provides a method for assessing a phenotype of an intact genetically modified cell comprising: a) providing the intact genetically modified cell comprising a target nucleic acid sequence less than 2.5 kilobases in length; b) contacting the intact genetically modified cell with a first plurality of probes, wherein each probe comprises a first detectable label and a probe sequence that binds to a portion of the target nucleic acid sequence; c) detecting a presence of the first detectable label in the intact cell, wherein the presence of the first detectable label indicates the presence of the target nucleic acid sequence; d) determining a phenotype of the intact genetically modified cell; and e) correlating the phenotype of the intact genetically modified cell with the presence of the target nucleic acid sequence. In some aspects, the intact genetically modified cell is a eukaryotic intact genetically modified cell. In some aspects, the phenotype is a product expressed due to a genetic modification in the intact genetically modified cell, a quality of the product expressed due to the genetic modification in the genetically modified cell, or a combination thereof. In some aspects, the phenotype is an increased or decreased expression of the product, an increase or decrease in the quality of the product, or a combination thereof. In some aspects, the method further comprises determining a number or location of genetic modifications in the intact genetically modified cell. In some aspects, the product expressed is a transgene protein, RNA, or a secondary product of the genetic modification. In some aspects, the method further comprises: f) selecting a first intact genetically modified cell comprising a phenotype of interest; g) determining a set of conditions used for a genetic modification of the first intact genetically modified cell; and h) preparing a second genetically modified cell using the set of conditions for genetic modification.

In various aspects, the present disclosure provides an *in situ* method of determining the localization of a regulatory element, the method comprising: a) contacting a regulatory element with a first set of detection agents; b) photobleaching the first set of detection agents for a first time point at a first wavelength to generate a second set of detection agents capable of generating a light at a second wavelength; c) detecting at least one burst generated by the second set of detection agents to generate a detection profile; and d) based on step c), analyzing the detection profile to determine the localization of the regulatory element. In some aspects, the first set of detection agent is a first set of fluorescently labeled probes.

In some aspects, the method further comprises hybridizing the first set of fluorescently labeled probes to a set of target sites on a regulatory element.

In some aspects, the second set of detection agent is a second set of fluorescently labeled probes. In some aspects, the fluorescent moieties of the first set of fluorescently labeled probes are the same.

In some aspects, the method further comprises a third set of fluorescently labeled probes. In some aspects, the third set of fluorescently labeled probes is photobleached to generate a fourth set of fluorescently labeled probes. In some aspects, the fluorescent moieties of the first set of fluorescently labeled probes are the same as the fluorescent moieties of the third set of fluorescently labeled probes. In some aspects, wherein the fluorescent moieties of the first set of fluorescently labeled probes are different than the fluorescent moieties of the third set of fluorescently labeled probes. In some aspects, wherein the third set of fluorescently labeled probes hybridizes to different target sites of the regulatory element from the first set of fluorescently labeled probes. In some aspects, the third set of fluorescently labeled probes hybridizes to different target sites of a different regulatory element from the first set of fluorescently labeled probes. In some aspects, the fluorescent moieties of the first set of fluorescently labeled probes are different than the fluorescent moieties of the third set of fluorescently labeled probes and the first set of fluorescently labeled probes hybridizes to different target sites from the third set of fluorescently labeled probes.

In some aspects, the method further comprises photobleaching the first set of fluorescently labeled probes for a first time point at a first wavelength and a third wavelength to generate a fourth set of fluorescently labeled probes capable of fluorescence at a fourth wavelength. In some aspects, the first wavelength and the third wavelength is applied simultaneously. In some aspects, the first wavelength and the third wavelength is applied sequentially. In some aspects, the first wavelength is at 491 nm light. In some aspects, the third wavelength is at 405 nm light. In some aspects, the fluorescent moiety comprises a fluorescent small molecule. In some aspects, the fluorescent moiety does not comprise a fluorescent protein. In some aspects, the detection profile comprises a chromatic aberration correction. In some aspects, the detection profile comprises less than 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, or 0% chromatic aberration. In some aspects, the localization of the regulatory element provides activity state of the regulatory element. In some aspects, the localization of the regulatory element provides interaction state with at least one additional regulatory element. In some aspects, the regulatory element comprises DNA, RNA, polypeptides, or a combination thereof. In some aspects, the regulatory element is DNA. In some aspects, the regulatory element is RNA. In some aspects, the RNA is an enhancer RNA (eRNA). In some aspects, the regulatory element is a DNaseI hypersensitive site (DHS).

In some aspects, the method further comprises: a) hybridizing a first set of fluorescently labeled probes to a set of target sites on a DHS in a cell sample; b) photobleaching the first set of fluorescently labeled probes for a first time point at a first wavelength to generate a second set of fluorescently labeled probes capable of fluorescence at a second wavelength; c) detecting at least one fluorescent burst generated by the second set of fluorescently labeled probes to generate a DHS profile; and d) comparing the DHS profile with a control set of DHS profiles, wherein a correlation between the DHS profile and the control set leads to identification of the cell type. In some aspects, the regulatory element is a polypeptide. In some aspects, the regulatory element comprises chromatin.

In various aspects, a kit is provided by the present disclosure, wherein the kit comprises a probe set and a set of instructions for the method of any of the methods as described herein.

## BRIEF DESCRIPTION OF THE DRAWINGS

Various aspects of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

FIG. 1 represents a conceptual illustration of methods described herein.

FIG. 2 illustrates a conceptual schematic of an exemplary computer server to be used for processing a method described herein.

FIG. 3A shows a two color SPDM image (experimental) of chromatin (blue) with DNA sensitive element sites (red), showing anti-colocalization of the DNA sensitive element sites with chromatin. Scale bars: 1000 nm, inserts: 100 nm. The bottom right panel shows chromatin (blue), the middle right panel shows DNA sensitive element sites (red), and the top right panel shows the overlay and the anti-colocalization of the DNA sensitive element with chromatin. FIG. 3B is the inset of FIG. 3A.

FIG. 4A and FIG. 4B illustrate the localization precision and nearest neighbor distances for DNA and DNase sensitive elements.

FIG. 5A and FIG. 5B illustrate multi-omics imaging via encoding of molecular information with ssDNA tags. FIG. 5A shows a schematic of simultaneous labeling and multiplexed imaging of mRNA and protein targets with multi-color QDots via DNA encoding. In general, each molecular target is encoded by target-specific ssDNA-tagged affinity molecule (e.g., an antibody, aptamer, oligonucleotide, etc.). The resulting array of target-bound ssDNA tags can be sequentially or simultaneously labeled by complementary imaging probes, enabling multiplexed imaging of all targets of interest (e.g., via fluorescence microscopy with hyperspectral imaging, HSI). FIG. 5B shows an exemplary multiplexed labeling of GAPDH and HSP90-alpha mRNA and corresponding proteins with QDots. DNA encoding methodology enables ssDNA tagging of mRNA targets via in situ hybridization and protein targets via immunorecognition by antibody-ssDNA bioconjugates. All ssDNA tags were simultaneously converted into distinctive optical signals by hybridization with complementary QDot-ssDNA' probes. Fluorescence microscopy with hyperspectral imaging (HSI) was employed for cell imaging and 4 individual QDot channels were unmixed. Individual grayscale channels were false-colored and merged into a composite 4-color image. Scale bar, 50  $\mu$ m.

FIG. 6 shows a workflow for target encoding and labeling via in situ hybridization, immunorecognition, and multi-omics procedures. DNA encoding methodology allows for labeling of different types of targets (mRNA and proteins in this proof-of-concept study) under conditions optimized for selective target binding in separate steps. As a result, all targets are converted into a uniform array of intermediate ssDNA tags, which are then simultaneously labeled by complementary QDot-ssDNA' probes for multiplexed imaging.

FIG. 7A and FIG. 7B illustrate a schematic and characterization of QDot-ssDNA probe preparation. FIG. 7A shows amine crosslinking by a homobifunctional reagent BS3 used for covalent conjugation of 5' amine-terminated ssDNA oligonucleotides and PEG-coated amine-functionalized QDots. ssDNA is activated by an excess BS3, purified by desalting, and reacted with QDots overnight. QDot-

ssDNA probes are purified from excess unbound ssDNA by ultrafiltration. Agarose gel electrophoresis in FIG. 7B shows an increase in QDot gel motility upon conjugation of negatively-charged ssDNA oligonucleotides, confirming successful preparation of QDot-ssDNA probes.

FIG. 8A and FIG. 8B show a schematic and characterization of antibody-ssDNA bioconjugate preparation via maleimide-mediated crosslinking. FIG. 8A shows rabbit anti-mouse IgG is partially reduced by treatment with TCEP to expose sulfhydryl groups for ssDNA conjugation. At the same time, 5' amine-terminated ssDNA oligonucleotides are activated by sulfo-SMCC. Mixing and a 4-hour incubation of activated ssDNA with reduced IgG yields  $\frac{1}{2}$ IgG-ssDNA bioconjugates. PAGE analysis of bioconjugation products in FIG. 8B confirmed formation of primarily  $\frac{1}{2}$ IgG with one ssDNA along with smaller fractions of  $\frac{1}{2}$ IgG conjugated to two and three ssDNA tags.

FIG. 9 illustrates evaluation of a 6-color QDot panel for protein labeling via DNA encoding. FIG. 9A shows specific staining of  $\beta$ -tubulin via incubation with mouse anti- $\beta$ -tubulin primary antibody and ssDNA-conjugated rabbit anti-mouse secondary antibody followed by immuno-labeling with anti-rabbit QDot655-2' Ab probes preserved functionality of 2' Ab-ssDNA bioconjugates. Consistent  $\beta$ -tubulin staining achieved via hybridization with complementary QDot-ssDNA probes in FIG. 9B confirmed successful preparation of a functional 6-color QDot-ssDNA panel. A lack of non-specific binding in FIG. 9C by QDot-ssDNA probes in control experiments that skipped incubation with primary and secondary antibodies corroborates the utility of such probes for highly specific target labeling via DNA encoding. True-color images for target staining (FIG. 9B) vs. control (FIG. 9C) were obtained at consistent exposure time for each QDot color. Scale bar, 50  $\mu$ m.

FIG. 10A, FIG. 10B, and FIG. 10C show a schematic and characterization of antibody-ssDNA bioconjugate preparation using the Thunder-Link oligo conjugation system. A 2-step amine crosslinking strategy as illustrated in FIG. 10A was employed for preparation of covalent antibody-ssDNA bioconjugates with intact IgG. Antibody and 5' amine-terminated ssDNA were simultaneously activated by respective activation reagents, purified via desalting, and reacted overnight, producing IgG with varying number of attached ssDNA tags. The reducing PAGE analysis of FIG. 10B highlights the presence of multiple higher-MW bands corresponding to heavy and light chains conjugated to varying number of ssDNA tags. In the four reaction conditions performed with goat anti-rabbit secondary antibodies, the relative volume ratios of activated IgG to ssDNA were 1) 50+50, 2) 50+30, 3) 50+20, and 4) 50+10. As expected, increasing amount of ssDNA in the reaction leads to more ssDNA tags being conjugated to each IgG molecule. In FIG. 10C, the staining of Lamin A via incubation with rabbit anti-Lamin A primary antibody and goat anti-rabbit 2' Ab-ssDNA bioconjugates followed by labeling with QDot605-ssDNA' probes confirmed the preserved specificity of ssDNA-tagged antibodies and successful antibody-ssDNA bioconjugation. At the same time, increasing non-specific binding by 2' Ab-ssDNA bioconjugates was observed with increasing number of ssDNA tags per IgG in a control experiment in which incubation with primary antibody was skipped. Thus, a volume ratio of Ab:ssDNA=2:1 in Thunder-Link reaction is considered optimal. All true-color images were obtained at consistent exposure for direct comparison of staining intensity. Scale bar, 250  $\mu$ m.

FIG. 11A, FIG. 11B, FIG. 11C, FIG. 11D, and FIG. 11E show multiplexed protein labeling via DNA encoding with

a panel of 1' antibody-ssDNA bioconjugates. Primary antibodies against HSP90-alpha, GAPDH, Lamin A, and  $\beta$ -tubulin were conjugated to ssDNA tags using Thunder-Link oligo conjugation system. Reducing PAGE shows consistent formation of IgG-ssDNA bioconjugates for all antibodies (FIG. 11A). Conventional 2-step immunofluorescence with unmodified antibodies and QDot565-2' Ab probes shows characteristic staining pattern for the 4 proteins of interest (FIG. 11B). Protein labeling in FIG. 11C with 1' Ab-ssDNA bioconjugates and QDot565-2' Ab probes yielded staining patterns consistent with the unmodified antibodies of FIG. 11B, confirming the preservation of antigen-binding functionality of 1' Ab-ssDNA. Single-color staining with 1' Ab-ssDNA bioconjugates and complementary QDot-ssDNA' probes further corroborates successful ssDNA conjugation and preparation of an antibody-ssDNA panel suitable for protein labeling via DNA encoding (FIG. 11D). Multiplexed staining via DNA encoding yielded consistent staining patterns for all four proteins in respective spectral channels of the same hyperspectral image (HSI) (FIG. 11E). Individual grayscale channels were false-colored for clarity. Scale bar, 50  $\mu$ m.

FIG. 12 shows characterization of mRNA labeling intensity and specificity via DNA encoding. GAPDH mRNA was labeled via indirect FISH procedure with 41 nt FISH probe set (see TABLE 5) followed by staining with QDot605-ssDNA probes (left panels) or AlexaFluor555-labeled streptavidin-ssDNA probes (right panels). Consistent characteristic punctuate staining pattern was observed with both complementary imaging probes (top row). At the same time, non-complementary probes (bottom row) failed to hybridize to mRNA in situ hybridization (ISH) probes, confirming staining specificity of the DNA encoding methodology. "Match" and "mismatch" true-color images were obtained at consistent exposure for direct comparison of staining intensity. Scale bar, 50  $\mu$ m.

FIG. 13A, FIG. 13B, FIG. 13C, and FIG. 13D illustrates the effect of a dsDNA spacer in an in situ hybridization (ISH) probe on mRNA labeling intensity. Physical separation of mRNA-recognition and QDot-binding portions of 41 nt ssDNA ISH probes with a 16 bp dsDNA spacer prevents formation of secondary structures, promotes hybridization to target mRNA, and reduces steric hindrance to QDot binding. As a result, a substantial increase in mRNA staining intensity was realized with such probes (FIG. 13A) in comparison to 41 nt ssDNA FISH probes (FIG. 13B). At the same time, longer 60 nt ssDNA probes without pre-hybridized dsDNA spacers experienced greater degree of secondary structure formation, which interfered with mRNA and QDot binding and failed to produce robust mRNA staining (FIG. 13C) above non-specific QDot binding levels (FIG. 13D). All images were obtained with HSI and normalized for direct comparison of signal intensity. Scale bar, 50  $\mu$ m.

FIG. 14 shows multi-omics QDot staining via DNA encoding. Protein and mRNA targets were encoded with ssDNA tags in separate steps, each using conditions optimal for binding of a specific target type. Consequently, DNA sequence code was converted into an optical signal by hybridization with complementary QDot-ssDNA probes. Specifically, GAPDH mRNA was labeled with a 41 nt in situ hybridization (ISH) probe set followed by labeling of  $\beta$ -tubulin with Ab-ssDNA bioconjugates. Finally, both ssDNA tags were simultaneously hybridized with respective QDot-ssDNA' probes. Clear microtubule staining pattern of  $\beta$ -tubulin (false-colored green) and punctuate pattern of GAPDH mRNA (false-colored red) were observed in dual-labeled specimen (top row), whereas only  $\beta$ -tubulin staining was

present in a control specimen that was not hybridized with GAPDH FISH probe set (bottom row). Nuclei were counterstained with DAPI (false-colored blue). Scale bar, 100  $\mu$ m.

FIG. 15 illustrates the heterogeneity in GAPDH RNAi following forward transfection with siRNA. Cells were seeded into a 24-well plate, allowed to attach, grown overnight, and then transfected with GAPDH siRNA (or non-targeting control siRNA) for 24 hrs. GAPDH mRNA was encoded via in situ hybridization (ISH) with mRNA ISH probes and then labeled with QDot605-ssDNA' probes. Imaging of different areas within the well highlights heterogeneity in GAPDH knock-down, likely resulting from heterogeneity in cell transfection with siRNA. Specifically, complete GAPDH mRNA degradation was observed throughout cells in the well center (top right panel), whereas cells at the crowded well edge still expressed regular levels of GAPDH mRNA (bottom right panel) consistent with GAPDH expression in cells transfected with control siRNA (left panels). Substantial number of non-transfected cells might explain an average silencing efficiency of 78% as determined by RT-PCR. Insets: control experiments showed lack of QDot non-specific binding in the absence of complementary ssDNA probes. All images were obtained with true-color camera at the same exposure time for direct comparison of signal intensity. Scale bar, 250  $\mu$ m.

FIG. 16 illustrates the heterogeneity in GAPDH RNAi following reverse transfection with siRNA. Cells were mixed with GAPDH siRNA (or non-targeting control siRNA) in suspension and then seeded to 24-well plate for transfection and growth for 24 hrs. GAPDH mRNA was encoded via in situ hybridization (ISH) with mRNA ISH probes and then labeled with QDot605-ssDNA' probes. As evident from imaging of different areas within the well, reverse transfection achieved a more uniform transfection and GAPDH knock-down compared to forward transfection (see FIG. 12). Complete GAPDH mRNA degradation was observed throughout majority of cells, with only occasional colonies with full GAPDH expression forming from non-transfected cells, which is consistent with an improved average silencing efficiency of 95% as determined by RT-PCR. Insets: control experiments showed lack of QDot non-specific binding in the absence of complementary ssDNA probes. All images were obtained with true-color camera at the same exposure time for direct comparison of signal intensity. Scale bar, 250  $\mu$ m.

FIG. 17 shows the comparison of RNAi effect on GAPDH mRNA expression following forward vs. reverse transfection with siRNA. Both transfection methods had no effect on GAPDH expression when non-targeting control siRNA was used (left panels) and yielded efficient GAPDH knock-down with GAPDH-targeting siRNA (middle panels), as evident from the lack of mRNA staining above non-specific QDot background (right panels). At the same time, small fraction of cells failed to get transfected and, as a result, expressed normal levels of GAPDH mRNA consistent with control experiments. This observation corroborates an all-on/all-off effect of RNAi regardless of the transfection method used. All images were obtained with hyperspectral imaging (HSI) and were normalized for direct comparison of signal intensity. Scale bar, 50  $\mu$ m.

FIG. 18 shows assessment of heterogeneity in cell transfection with siRNA. Dual-labeling of GAPDH and HSP90-alpha mRNA with QDots enables direct visualization of siRNA transfection effect at a single-cell level. Cells were either grown under regular culture conditions (FIG. 18A, FIG. 18B, and FIG. 18C), transfected with control non-targeting siRNA (FIG. 18D, FIG. 18E, and FIG. 18F), or

transfected with GAPDH-targeting siRNA (FIG. 18G, FIG. 18H, and FIG. 18I). After a 24-hour treatment with GAPDH siRNA, the majority of cells had completely degraded GAPDH mRNA, as evident from the lack of GAPDH mRNA staining (FIG. 18G). At the same time, HSP90-alpha mRNA not targeted by RNAi machinery remained unperturbed (FIG. 18H). Interestingly, a single cell in the field of view failed to transfect with GAPDH siRNA (FIG. 18G, FIG. 18H, and FIG. 18I), expressing regular levels of GAPDH mRNA consistent with cells treated with control siRNA (FIG. 18D, FIG. 18E, and FIG. 18F) and reference cells not transfected with siRNA (FIG. 18A, FIG. 18B, and FIG. 18C), suggesting an all-on/all-off effect of RNAi. Dual-color images were obtained with hyperspectral imaging (HSI) and were unmixed in QDot channels. Panels for individual channels (FIG. 18A, FIG. 18B, FIG. 18D, FIG. 18E, FIG. 18G, and FIG. 18H) were normalized for direct comparison of signal intensity. In merged 2-color images (FIG. 18C, FIG. 18F, and FIG. 18I) The GAPDH channel was false-colored green and the HSP90-alpha channel was false-colored red. Scale bar, 50  $\mu$ m.

FIG. 19 shows assessment of GAPDH RNAi heterogeneity at mRNA and protein levels with multi-omics imaging. Dual labeling of GAPDH mRNA and protein 24 hrs post-transfection with GAPDH-targeting siRNA highlights heterogeneity in mRNA expression levels (bottom left panel) along with the lack of RNAi effect on the protein level (bottom middle panel) at this time point. Transfection with non-targeting control siRNA (top row) failed to affect GAPDH expression, yielding uniform mRNA and protein staining throughout all cells. Dual-color images were obtained with hyperspectral imaging (HSI), and individual channels were normalized for direct comparison of signal intensity. The GAPDH mRNA channel was false-colored red and the GAPDH protein channel was false-colored green in a composite 2-color image. Scale bar, 50  $\mu$ m.

FIG. 20A and FIG. 20B show assessment of disparity in RNAi kinetics at mRNA and protein levels. HeLa cells were transfected with GAPDH siRNA for 24 hours (FIG. 20A) and 48 hours (FIG. 20B). GAPDH and HSP90-alpha mRNA, along with corresponding proteins, were simultaneously assessed with QDot-based multi-omics imaging methodology. Consistent with mRNA-only analysis, multi-omics imaging highlights complete and selective degradation of GAPDH mRNA 24 hours post-transfection, whereas GAPDH protein level remained nearly unperturbed (FIG. 20A). Lagging mRNA knock-down 48 hours post-transfection selective degradation of GAPDH protein was observed (FIG. 20B). All grayscale images were normalized to HSP90 protein channel for direct comparison of staining intensities. In a merged 4-color image the GAPDH protein channel was false-colored yellow, the HSP90-alpha protein channel was false-colored blue, the GAPDH mRNA channel was false-colored green, and the HSP90-alpha mRNA channel was false-colored red. Scale bar, 50  $\mu$ m.

FIG. 21A and FIG. 21B show multi-omics evaluation of GAPDH and HSP90-alpha expression at mRNA and protein levels under regular cell culture conditions. To provide a reference of normal GAPDH and HSP90 expression levels to RNAi experiments, cells were grown under regular cell culture conditions for 24 hrs (FIG. 21A) and 48 hrs (FIG. 21B). All targets of interest were labeled via a 2+2 encoding procedure to produce a 4-plex staining. Consistent with expected fast growth of HeLa cells, cell density increased with time. However, GAPDH and HSP90 expression remained constant through 48 hrs of incubation, as evident from consistent intensity of mRNA and protein labeling.

Multiplex images were obtained with hyperspectral imaging (HSI), and individual channels were normalized for direct comparison of signal intensity. The GAPDH mRNA channel was false-colored green, the HSP90 mRNA channel was false-colored red, the GAPDH protein channel was false-colored yellow, and the HSP90 protein channel was false-colored blue in a composite 4-color image. Scale bar, 50  $\mu$ m.

FIG. 22A and FIG. 22B show multi-omics evaluation of GAPDH and HSP90-alpha expression at mRNA and protein levels following transfection with a control (non-targeting) siRNA. To assess an effect of transfection on molecular expression profiles in reference to GAPDH RNAi experiments, cells were reverse transfected with non-targeting control siRNA for (FIG. 22A) 24 hrs and (FIG. 22B) 48 hrs. All targets of interest were labeled via a 2+2 encoding procedure to produce a 4-plex staining. Consistent with expected lack of RNAi with control siRNA, GAPDH and HSP90 expression remained constant through 48 hrs of incubation, as evident from consistent intensity of mRNA and protein labeling. Multiplex images were obtained with hyperspectral imaging (HSI), and individual channels were normalized for direct comparison of signal intensity. The GAPDH mRNA channel was false-colored green, the HSP90 mRNA channel was false-colored red, the GAPDH protein channel was false-colored yellow, and the HSP90 protein channel was false-colored blue in a composite 4-color image. Scale bar, 50  $\mu$ m.

FIG. 23A and FIG. 23B show direct visualization of the effect and kinetics of GAPDH RNAi via single-plex labeling of individual protein and mRNA targets. To eliminate any potential effect of multi-omics labeling methodology and artifacts of hyperspectral (HSI) analysis, the GAPDH RNAi sample along with a reference sample and a control sample were performed on separate specimens in parallel (different wells of the same 24-well plate), followed by a single-plex labeling of individual targets and direct true-color imaging under consistent imaging conditions. Cells were reverse transfected for 24 hrs (FIG. 23A) and 48 hrs (FIG. 23B) prior to fixation and staining. Consistent with multi-omics analysis, single-plex imaging confirmed efficient and specific degradation of GAPDH mRNA within 24 hrs post-transfection, whereas the RNAi effect on GAPDH protein level can be observed only 48 hrs post-transfection. Scale bar, 50  $\mu$ m.

FIG. 24 shows the labeling of DNaseI cut sites in a cell's nucleus using a terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) assay.

FIG. 25 shows a schematic of a detection agent comprising a probe, a detectable moiety, and a conjugating moiety.

FIG. 26 shows a flowchart for a method of detecting a nucleic acid sequence.

FIG. 27 shows a flowchart for a method of determining the spatial position of a nucleic acid sequence.

FIG. 28 shows a flowchart for a method of detecting the sequence position of a nucleic acid sequence.

FIG. 29 shows a flowchart for a method of detecting a nucleic acid in a sample relative to a control.

FIG. 30 shows a flowchart for a method of fluorescently detecting a target nucleic acid sequence.

FIG. 31 shows a flowchart for a method of analyzing a fluorescence image of one or more target nucleic acid sequences.

FIG. 32 illustrates a conceptual schematic of an exemplary computer server to be used for processing one or more methods described herein.

FIG. 33 shows the use of Nano-FISH to detect a 1.8 kb nucleic acid sequence. FIG. 33A shows a schematic of the

Nano-FISH experiment. FIG. 33B shows the application of the Nano-FISH strategy to detect a 1.8 kb region encompassing the HS2 hypersensitive site of the  $\beta$ -globin locus control region (LCR) in triploid K562 erythroleukemia cells. FIG. 33C shows colocalization of the Nano-FISH signals (~1.8 kb target region) with those from standard BAC-derived probes (conventional DNA-FISH; ~170 kb target region), confirming the specificity of the detected Nano-FISH signal. FIG. 33D shows the efficiency and resolution of detection using Nano-FISH may be tuned according to the number of probes being used. FIG. 33E shows a comparison of the size of detected FISH spots between conventional FISH, pooled HS1-5 probes, and HS2 Nano-FISH. FIG. 33F shows a comparison of the intensity of detected FISH signals between conventional FISH, pooled HS1-5 probes, and HS2 Nano-FISH. FIG. 34G shows Nano-FISH detected for genomic regions with varying size, such as a genomic region size ranging from about 800 bp to 2.1 kb.

FIG. 34 shows the use of Nano-FISH to perform fine structural analysis of specific genomic loci within the nucleus. FIG. 34A shows the distinct spots produced by Nano-FISH probes targeting specific loci on these chromosomes. To measure the relative localization of the detected loci, the relative radial distance (RRD), a normalized measure of the position of the detected spot with respect to the nuclear centroid, was calculated. FIG. 34B shows a schematic of the relative radial distance. FIG. 34C shows that the chromosome 18 Nano-FISH signals are closer to the nuclear periphery. The distributions were obtained across 2,396 chromosome 18 signals and 3,388 chromosome 19 signals. FIG. 34D shows radial histograms of the two target loci. The differences in the distribution of signals with respect to the nuclear centroid are readily apparent in the histograms.

FIG. 35 shows the use of Nano-FISH for examining the interaction of a gene enhancer with its target gene promoter. FIG. 35A shows two-color Nano-FISH in 786-O and MCF-7 cells. The normalized inter-spot distance (NID) between these two genomic loci were compared. FIG. 35B shows a schematic of the normalized inter-spot distance. FIG. 35C shows that, on average, the spots are situated closer together in 786-O cells compared to MCF-7 cells. FIG. 35D shows that, in spite of this, absolute colocalization (NID=0) was actually a rare event in both cell types.

FIG. 36 shows the use of Nano-FISH to detect small genomic structural variations such as small losses or gains of DNA. ZFN-mediated genome editing was used to generate a triploid homozygous deletion of the  $\beta$ -globin locus control region (LCR, ~18 kb) in K562 cells, as shown in FIG. 36A. Cells imbued with this deletion are referred to as  $\Delta$ LCR. Probes targeting either the HS2 or HS3 hypersensitive sites within the deleted region were utilized to detect loss of LCR in the genome edited cells, as shown in FIG. 36B and FIG. 36C. For the converse scenario, using TALEN-mediated homology directed repair, a sequence encoding for eGFP was inserted into the AAVS1 safe harbor locus on chromosome 19, as shown in FIG. 36D. This exogenously-derived sequenced was readily identified by Nano-FISH, as shown in FIG. 36E and FIG. 36F.

FIG. 37 shows the combination of Nano-FISH and super-resolution microscopy to obtain very fine-scale genome localization. FIG. 37A shows that these closely apposed loci are readily discernible as distinct spots by STED microscopy. Pair-wise measurements of other closely situated genomic segments such as HS1-HS4 (~12 kb) and HS2-HGB2 (~25 kb) were also readily obtained and revealed non-linear compaction of the  $\beta$ -globin locus control region and the surrounding genome which contains its target genes,

as shown in FIG. 37B. Importantly, the high-throughput STED microscopy approach enables calculation of the distribution of actual distances between these various loci, as shown in FIG. 37C.

FIG. 38 shows a series of experiments to determine the optimal operating parameters for a Nano-FISH experiment. FIG. 38A shows how the labeling efficiency of the Nano-FISH procedure depends on denaturation temperature. With increasing temperature, the efficiency of Nano-FISH labeling increases, until a plateau is reached at a temperature of 78° C. FIG. 38B shows that the Nano-FISH labeling procedure is repeatable across experiments. FIG. 38C shows Nano-FISH detected for genomic regions with varying size, such as a genomic region size ranging from about 800 bp to 2.1 kb. FIG. 38D shows how the labeling efficiency of the Nano-FISH experiment depends on the number of oligo probes used. The labeling efficiency increases with the number of oligo probes used, attaining a maximum efficiency when 30 oligo probes are utilized. FIG. 38E shows how the detected fluorescence spot size depends on the number of oligo probes. FIG. 38F shows how the intensity of the fluorescence spot size depends on the number of oligo probes.

FIG. 39 shows a comparison of Nano-FISH and conventional FISH. FIG. 39A shows fluorescence images of  $\beta$ -globin lacking the LCR using conventional BAC probes (left panel), a pool of HS1-5 probes (middle panel), and the HS2 Nano-FISH technique (right panel). FIG. 39B shows the size of the probe sets used for the BAC, HS1-5, and HS2 experiments. As can be seen, the HS2 Nano-FISH experiment utilizes a significantly smaller nucleic acid sequence than conventional FISH techniques. FIG. 39C shows the labeling efficiency of the BAC, HS1-5, and HS2 experiments. FIG. 39D shows the size of the FISH spots for the BAC, HS1-5, and HS2 experiments. FIG. 39E shows the intensity of the FISH signals for the BAC, HS1-5, and HS2 experiments.

#### DETAILED DESCRIPTION OF THE INVENTION

Cellular activation and extinction patterns can encode information on cell identity, maturation state, cellular memory, and disease state. Tissues are composites of cells which can have one or more morphologically distinct cell types. In some instances, all of the cells in a tissue are processed simultaneously, yielding compounded information with limited sensitivity for cellular activities and/or rare cell types. Alternative approaches employ disaggregation and sorting of tissue components but in the process can destroy cellular architecture and potentially introduce artifacts such as biological stressors and perturbations.

Described herein are methods of detecting a cellular regulatory element in situ utilizing a super-resolution microscopy technique to determine the presence, absence, and/or activity of a regulatory element. Also described herein are methods of detecting different types of regulatory elements simultaneously utilizing a heterogeneous set of detection agents, and translating the molecular information from the different types of regulatory elements to determine the activity state of a cell. The activity state of a cell may correlate to a localization, expression level, and/or interaction state of a regulatory element. One or more of the methods described herein may further interpolate 2-dimensional images to generate 3-dimensional maps which enable detection of localization, interaction states, and activity of one or more regulatory elements. Intrinsic properties such as

size, intensity, and location of a detection agent further may enable detection of a regulatory element. Described herein are methods of determining the localization of a regulatory element and measuring the activity of a regulatory element. The methods provided herein may avoid the introduction of artifacts such as biological stressors and perturbations or destroys cellular architecture. Exemplary properties associated with the methods described herein are illustrated in FIG. 1.

One or more methods described herein may detect different types of regulatory elements, distinguish between different types of regulatory elements, and/or generate a map of a regulatory element (e.g., chromatin). For example, a regulatory element may be labeled by one or more different types of detection agents. The one or more different types of detection agents may include DNA detection agents, RNA detection agents, protein detection agents, or combinations thereof. The detection agent may comprise a probe portion, which may interact (e.g., hybridize) to a target site within the regulatory element, and optionally comprise a detectable moiety. The detectable moiety may include a fluorophore, such as a fluorescent dye or a quantum dot. The detection agent may be an unlabeled probe which can be further conjugated to an additional labeled probe. Upon labeling, the regulatory element may be detected by stochastic or deterministic super-resolution microscopy method. The stochastic super-resolution microscopy method may be a synthetic aperture optics (SAO) method. The SAO method may generate a detection profile, which can encompass fluorescent signal intensity, size, shape, or localization of the detection agent. Based on the detection profile, the activity state, the localization, expression level, and/or interaction state of the regulatory element may be determined. A map based on the detection profile of the regulatory element may also be generated, and may be correlated to cell type identification (e.g., cancerous cell identification). The regulatory element may be further analyzed in the presence of an exogenous agent or condition, such as a small molecule fragment or a drug, or under an environment such as a change in temperature, pH, nutrient, or a combination thereof. The perturbation of the activity state of the regulatory element in the presence of the exogenous agent or condition may be measured. A report may further be generated and provided to a user, such as a laboratory clinician or health care provider.

The systems and methods disclosed herein also relate to a novel FISH methodology (hereinafter referred to as "Nano-FISH") to reliably label and detect localized small (less than 12 kb in size) DNA segments in cells. In some cases, Nano-FISH utilizes defined pools of synthetic fluorescent dye-labeled oligonucleotides to reliably detect small genomic regions in large numbers of adherent or suspension cells in situ. In some instances, Nano-FISH is conducted utilizing conventional wide-field microscopic imaging. In other embodiments, Nano-FISH is conducted using super-resolution imaging techniques.

In some cases, Nano-FISH is coupled with an automated image informatics pipeline to enable high-throughput detection and 2D and/or 3D spatial localization of small genomic DNA elements in situ in hundreds of, thousands of, or more individual cells per experiment. In some instances, to facilitate rigorous statistical analyses of the resulting large image data sets, a scalable image analysis software suite reliably identifies and quantitatively annotates labeled loci on a single-cell basis.

In some cases, Nano-FISH allows detection of the precise localization of specific regulatory genomic elements in 3D

nuclear space, the identification of small-scale structural genomic variations (such as sequence gains or losses), the quantitation of spatial interactions between regulatory elements and their putative target gene(s), or the detection of genomic conformational changes that induce stimulus-dependent gene expression. In some instances, Nano-FISH allows the visualization of the precise localization of a target nucleic acid sequence. The target nucleic acid sequence can be an endogenous nucleic acid sequence, a nucleic acid sequence derived from an exogenous source, or a combination thereof. An exogenous target nucleic acid sequence may be introduced to a cell through electroporation, lipofection, transfection, microinjection, viral transduction, or a gene gun. Non-limiting examples of vector systems that can be used to introduce a target nucleic acid sequence into a cell may include viral vector, episomal vector, naked RNA (recombinant or natural), naked DNA (recombinant or natural), bacterial artificial chromosome (BAC), and RNA/DNA hybrid systems used separately or in combination. Vector systems may be used without additional reagents meant to aid in the incorporation and/or expression of desired mutations. A non-limiting list of reagents meant to aid in the incorporation and/or expression of desired mutations may include Lipofectamine, FuGENE, FuGENE HD, calcium phosphate, HeLaMONSTER, Xtreme Gene. An endogenous nucleic acid sequence may be a gene sequence or fragment thereof. An endogenous nucleic acid sequence may be a sequence in a chromosome. An endogenous nucleic acid sequence may be a nucleic acid sequence resulting from somatic chromosomal rearrangement, such as the nucleic acid sequence of a B cell receptor, T cell receptor, or fragment thereof. In some instances, Nano-FISH allows the detection of the precise localization of exogenous nucleic acids inserted or integrated into a genome. In some embodiments, Nano-FISH allows the detection of the precise localization of exogenous DNA inserted into a genome, as may be inserted by a genetic engineering technique. In some instances, Nano-FISH allows the detection of an episomal nucleic acid sequence.

The systems and methods described herein may be useful in detecting or determining the presence, absence, identity, or quantity of a target nucleic acid sequence in a sample. In particular, the methods, compositions, and systems described herein may be used to efficiently detect, to identify, and to quantify a target nucleic acid sequence that is a short nucleic acid sequences. In some cases, a short nucleic acid sequence that may be detected or quantified using the disclosures of the present application may be from 1 kilobase (kb) in length to about 12 kb in length. A short nucleic acid sequence may be less than 1 kb. A short nucleic acid sequence may be less than 12 kb, less than 11 kb, less than 10 kb, less than 9 kb, less than 8 kb, less than 7 kb, less than 6 kb, less than 5 kb, less than 4 kb, less than 3 kb, less than 2.5 kb, less than 2 kb, less than 1.5 kb, less than 1.2 kb, less than 0.8 kb, or less than 0.5 kb. A short nucleic acid sequence may be from 240 nucleotides to 1 kb in length. A short nucleic acid sequence may be from 360 nucleotides to 1 kb in length. A short nucleic acid sequence may be from 240 nucleotides to 2 kb, 15 nucleotides to 2.5 kb, 240 nucleotides to 3 kb, 15 nucleotides to 4 kb, 240 nucleotides to 5 kb, 15 nucleotides to 6 kb, 240 nucleotides to 7 kb, 240 nucleotides to 8 kb, 240 nucleotides to 9 kb, 15 nucleotides to 10 kb, 240 nucleotides to 11 kb, or 240 nucleotides to 12 kb in length. A short nucleic acid sequence may be from 360 nucleotides to 2 kb, 360 nucleotides to 2.5 kb, 360 nucleotides to 3 kb, 360 nucleotides to 4 kb, 360 nucleotides to 5 kb, 360 nucleotides to 6 kb, 360 nucleotides to 7 kb, 360 nucleotides

to 8 kb, 360 nucleotides to 9 kb, 360 nucleotides to 10 kb, 360 nucleotides to 11 kb, or 360 nucleotides to 12 kb in length.

Methods for the detection, identification, and/or quantification of a short nucleic acid sequence of a sample may comprise contacting the short nucleic acid sequence with a probe comprising a detectable label and determining the presence, absence, or quantity of probes bound to the target nucleic acid sequence. Determination of the sequence position of the short nucleic acid sequence relative to other nucleotides or another short nucleic acid sequence (for instance, using a second probe capable of binding to a second target sequence of the nucleic acid) may be a step in the methods described herein. The methods described herein may also comprise determining the spatial position of the short nucleic acid sequence. For example, Nano-FISH may be used to measure the normalized inter-spot distance between a first short nucleic acid sequence encoding an enhancer or portion thereof and a second nucleic acid encoding a promoter of a gene or portion thereof, which may be used to study changes in genome conformation that may be associated with gene function.

The methods described herein may comprise comparing the presence, absence, spatial position, sequence position, or quantity of a short nucleic acid sequence of a sample to a reference value. A non-limiting example of quantifying detection of a short nucleic acid sequence in a cell may comprise quantifying the number of copies of a nucleic acid sequence that has been incorporated into a modified cell (for example, a cell modified by the introduction of a nucleic acid sequence into the cell by genetic editing), which may be used as quality control for modified cells produced by cell engineering strategies.

Also described herein are methods, compositions, and systems useful in characterizing and/or quantifying the presence, absence, position, or identity of a target nucleic acid sequence in a cell or sample derived therefrom relative to a reference nucleic acid sequence in the same cell or sample or relative to a control cell or sample. For example, improvements to the efficiency of detection and to a detection threshold, as described herein, may allow for the detection and characterization of short nucleic acid sequences (for instance, non-repeating nucleic acid sequence insertions) during analysis or validation of cell samples or cell lines.

Additionally, described herein, are methods, compositions, and systems for correlating protein expression with target nucleic acid sequence detection. For example, a target nucleic acid sequence may be associated with the expression of a target protein. Using Nano-FISH, the presence, absence, or quantity of the target nucleic acid sequence may be detected, and a detectable label may be used to detect a target protein expression, which therefore may allow for the correlation between the presence, absence, or quantity of the target nucleic acid sequence and the expression of the target protein.

#### Types of Regulatory Elements

A regulatory element may be DNA, RNA, a polypeptide, or a combination thereof. A regulatory element may be DNA. A regulatory element may be RNA. A regulatory element may be a polypeptide. A regulatory element may be any combination of DNA, RNA, and/or polypeptide (e.g., protein-protein complexes, protein-DNA/RNA complexes, and the like).

A regulatory element may be DNA. A regulatory element may be a single-stranded DNA regulatory element, a double-stranded DNA regulatory element, or a combination thereof.

The DNA regulatory element may be single-stranded. The DNA regulatory element may be double-stranded. The DNA regulatory element may encompass a DNA fragment. The DNA regulatory element may encompass a gene. The DNA regulatory element may encompass a chromosome. The DNA regulatory element may include endogenous DNA regulatory elements (e.g., endogenous genes). The DNA regulatory element may include artificial DNA regulatory elements (e.g., foreign genes introduced into a cell).

A regulatory element may be RNA. A regulatory element may be a single-stranded RNA regulatory element, a double-stranded RNA regulatory element, or a combination thereof. The RNA regulatory element may be single-stranded. The RNA regulatory element may be double-stranded. The RNA regulatory element may include endogenous RNA regulatory elements. The RNA regulatory element may include artificial RNA regulatory elements. The RNA regulatory element may include microRNA (miRNA), transfer RNA (tRNA), ribosomal RNA (rRNA), messenger RNA (mRNA), pre-mRNA, transfer-messenger RNA (tmRNA), heterogeneous nuclear RNA (hnRNA), short interfering RNA (siRNA), or short hairpin RNA (shRNA). The RNA regulatory element may be a RNA fragment. The RNA regulatory element may be an anti-sense RNA.

An RNA regulatory element may be an enhancer RNA (eRNA). An enhancer RNA may be a non-coding RNA molecule transcribed from an enhancer region of a DNA molecule, and may be from about 50 base-pairs (bp) in length to about 3 kilo base pairs in length (e.g., about 100 bp in length, about 200 bp in length, about 500 bp in length, about 1 kb in length, about 1.5 kb in length, about 2 kb in length, or about 2.5 kb in length). An enhancer RNA may be a 1D eRNA or an eRNA that may be unidirectionally transcribed. An enhancer RNA may also be a 2D eRNA or an eRNA that may be bidirectionally transcribed. An eRNA may be polyadenylated. Alternatively, an eRNA may be non-polyadenylated.

A regulatory element may be a DNaseI hypersensitive site (DHS). DHS may be a region of chromatin unoccupied by transcription factors and which is sensitive to cleavage by the DNase I enzyme. The presence of DHS regions within a chromatin may demarcate transcription factory occupancy at a nucleotide resolution. The presence of DHS regions may further correlate with activation of cis-regulatory elements, such as an enhancer, promoter, silencer, insulator, or locus control region. DHS variation may be correlated to variation in gene expression in healthy or diseased cells (e.g., cancerous cells) and/or correlated to phenotypic traits.

A DHS pattern may encode memory of prior cell fate decisions and exposures. For example, upon differentiation, a DHS pattern of a progeny may encode transcription factor occupancy of its parent. Further, a DHS pattern of a cell may encode an environmentally-induced transcription factor occupancy from an earlier time point.

A DHS pattern may encode cellular maturity. An embryonic stem cell may encode a set of DHSs that may be transmitted combinatorially to a differentiated progeny, and this set of DHSs may be decreased with each cycle of differentiation. As such, the set of DHSs may be correlated with time, thereby allowing a DHS pattern to be correlated with cellular maturity.

A DHS pattern may also encode splicing patterns. Protein coding exons may be occupied by transcription factors, which may further be correlated with codon usage patterns and amino acid choice on evolutionary time scales and human fitness. A transcription factory occupancy may further modulate alternative splicing patterns, for example, by

imposing sequence constraints at a splice junction. As such, a DHS pattern may encode transcription factor occupancy of one or more exons of interest and may provide additional information on alternative splicing patterns.

A DHS pattern may encode a cell type. For example, within each cell type, about 100,000 to about 250,000 DHSs may be detected. About 5% of the detected DHSs may be located within a transcription start site and the remaining DHSs may be detected at a distal site from the transcription start site. Each cell type may contain a distinct DHS pattern at the distal site and mapping the DHS pattern at the distal site may allow identification of a cell type. An overlap may further be present within two DHS patterns from two different cell types, for example, an overlap of a set of detected DHSs within the two DHS patterns. An overlap may be less than about 70%, less than about 65%, less than about 60%, less than about 55%, less than about 50%, less than about 45%, less than about 40%, less than about 35%, less than about 30%, less than about 25%, less than about 20%, less than about 15%, less than about 10%, less than about 9%, less than about 8%, less than about 7%, less than about 6%, less than about 5%, less than about 4%, less than about 3%, less than about 2%, or less than about 1% of the detected DHSs. The presence of an overlap may not affect the identification of a cell type.

A regulatory element may be a polypeptide. The polypeptide may be a protein or a polypeptide fragment. For example, a regulatory element may be a transcription factor, DNA-binding protein or functional fragment, RNA-binding protein or functional fragment, protein involved in chemical modification (e.g., involved in histone modification), or gene product. A regulatory element may be a transcription factor. A regulatory element may be a DNA or RNA-binding protein or functional fragment. A regulatory element may be a product of a gene transcript. A regulatory element may be a chromatin.

#### Methods of Detecting a Regulatory Element

Described herein is a method of detecting a regulatory element. The detection may encompass identification of the regulatory element, determining the presence or absence of the regulatory element, and/or determining the activity of the regulatory element. A method of detecting a regulatory element may include contacting a cell sample with a detection agent, binding the detection agent to the regulatory element, and analyzing a detection profile from the detection agent to determine the presence, absence, or activity of the regulatory element.

The method may involve utilizing one or more intrinsic properties associated with a detection agent to aid in detection of the regulatory element. The intrinsic properties may encompass the size of the detection agent, the intensity of the signal, and the location of the detection agent. The size of the detection agent may include the length of the probe and/or the size of the detectable moiety (e.g., the size of a fluorescent dye molecule) may modulate the specificity of interaction with a regulatory element. The intensity of the signal from the detection agent may correlate to the sensitivity of detection. For example, a detection agent with a molar extinction coefficient of about  $0.5\text{-}5\times 10^6\text{ M}^{-1}\text{cm}^{-1}$  may have a higher intensity signal relative to a detection agent with a molar extinction coefficient outside of the  $0.5\text{-}5\times 10^6\text{ M}^{-1}\text{cm}^{-1}$  range and may have lower attenuation due to scattering and absorption. Further, a detection agent with a longer excited state lifetime and a large Stoke shift (measured by the distance between the excitation and emission peaks) may further improve the sensitivity of detection. The location of the detection agent may, for example,

provide the activity state of a regulatory element. A combination of intrinsic properties of the detection agent may be used to detect a regulatory element of interest.

A detection agent may comprise a detectable moiety that is capable of generating a light, and a probe portion that is capable of hybridizing to a target site on a regulatory element. As described herein, a detection agent may include a DNA probe portion, an RNA probe portion, a polypeptide probe portion, or a combination thereof. Sometimes, a DNA or RNA probe portion may be between about 10 and about 100 nucleotides in length, between about 15 and about 100 nucleotides in length, between about 20 and about 100 nucleotides in length, between about 20 and about 80 nucleotides in length, between about 20 and about 60 nucleotides in length, between about 25 and about 55 nucleotides in length, between about 30 and about 50 nucleotides in length, between about 15 and about 80 nucleotides in length, between about 15 and about 60 nucleotides in length, between about 20 and about 40 nucleotides in length, or between about 20 and about 30 nucleotides in length. Sometimes, a DNA or RNA probe portion may be about 10, about 15, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36, about 37, about 38, about 39, about 40, about 45, about 50, about 55, about 60, about 65, about 70, about 80, about 90, or more nucleotides in length. A DNA or RNA probe portion may be a TALEN probe, ZFN probe, or a CRISPR probe. A DNA or RNA probe portion may be a padlock probe. A polypeptide probe may comprise a DNA-binding protein, a RNA-binding protein, a protein involved in the transcription/translation process, a protein that detects the transcription/translation process, a protein that may detect an open or relaxed portion of a chromatin, or a protein interacting partner of a product of a regulatory element (e.g., an antibody or binding fragment thereof).

A detection agent may comprise a DNA or RNA probe portion which may be between about 10 and about 100 nucleotides in length, between about 15 and about 100 nucleotides in length, between about 20 and about 100 nucleotides in length, between about 20 and about 80 nucleotides in length, between about 20 and about 60 nucleotides in length, between about 25 and about 55 nucleotides in length, between about 30 and about 50 nucleotides in length, between about 15 and about 80 nucleotides in length, between about 15 and about 60 nucleotides in length, between about 20 and about 40 nucleotides in length, or between about 20 and about 30 nucleotides in length. A detection agent may comprise a DNA or RNA probe portion which may be about 10, about 15, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36, about 37, about 38, about 39, about 40, about 45, about 50, about 55, about 60, about 65, about 70, about 80, about 90, about 100, or more nucleotides in length.

A detection agent may comprise a DNA or RNA probe selected from a TALEN probe, a ZFN probe, or a CRISPR probe.

A set of detection agents may be used to detect a regulatory element. The set of detection agents may comprise about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 25, about 30, about 35, about 40, about 45, about 50, or more detection agents. Each of the detection agents within

the set of detection agents may recognize and interact with a distinct region of a regulatory element. Sometimes, about 1, about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, or more detection agents may be used for detection of a regulatory element. About 1 or more detection agents may be used for detection of a regulatory element. About 2 or more detection agents may be used for detection of a regulatory element. About 3 or more detection agents may be used for detection of a regulatory element. About 4 or more detection agents may be used for detection of a regulatory element. About 5 or more detection agents as used for detection of a regulatory element. About 6 or more detection agents may be used for detection of a regulatory element. About 7 or more detection agents may be used for detection of a regulatory element. About 8 or more detection agents may be used for detection of a regulatory element. About 9 or more detection agents may be used for detection of a regulatory element. About 10 or more detection agents may be used for detection of a regulatory element. About 11 or more detection agents may be used for detection of a regulatory element. About 12 or more detection agents may be used for detection of a regulatory element. About 13 or more detection agents may be used for detection of a regulatory element. About 14 or more detection agents may be used for detection of a regulatory element. About 15 or more detection agents may be used for detection of a regulatory element. About 20 or more detection agents may be used for detection of a regulatory element.

A detection agent may comprise a polypeptide probe selected from a DNA-binding protein, a RNA-binding protein, a protein involved in the transcription/translation process, a protein that detects the transcription/translation process, a protein that may detect an open or relaxed portion of a chromatin, or a protein interacting partner of a product of a regulatory element (e.g., an antibody or binding fragment thereof).

A detectable moiety that is capable of generating a light may be directly conjugated or bound to a probe portion. A detectable moiety may be indirectly conjugated or bound to a probe portion by a conjugating moiety. As described herein, a detectable moiety may be a small molecule (e.g., a dye) which may be directly conjugated or bound to a probe portion. A detectable moiety may be a fluorescently labeled protein or molecule which may be attached to a conjugating moiety (e.g., a hapten group, an azido group, an alkyne group) of a probe.

A profile or a detection profile or signature may include the signal intensity, signal location, or size of the signal of the detection agent. The profile or the detection profile may comprise about 100 image frames, about 500 frames, about 1000 frames, about 2000 frames, about 5000 frames, about 10,000 frames, about 20,000 frames, about 30,000 frames, about 40,000 frames, about 50,000 frames, or more frames. Analysis of the profile or the detection profile may determine the activity of the regulatory element. The degree of activation may also be determined from the analysis of the profile or detection profile. Analysis of the profile or the detection profile may further determine the optical isolation and localization of the detection agents, which may correlate to the localization of the regulatory element.

In additional cases, a detection agent may comprise a polypeptide probe selected from a DNA-binding protein, a RNA-binding protein, a protein involved in the transcription/translation process or detects the transcription/translation process, a protein that may detect an open or relaxed

portion of a chromatin, or a protein interacting partner of a product of a regulatory element (e.g., an antibody or binding fragment thereof).

Sometimes, a detectable moiety that is capable of generating a light is directly conjugated or bound to a probe portion. Other times, a detectable moiety is indirectly conjugated or bound to a probe portion by a conjugating moiety. As described elsewhere herein, a detectable moiety may be a small molecule (e.g., a dye) which may be directly conjugated or bound to a probe portion. Alternatively, a detectable moiety may be a fluorescently labeled protein or molecule which may be attached to a conjugating moiety (e.g., a hapten group, an azido group, an alkyne group) of a probe.

In some instances, a profile or a detection profile or signature may include the signal intensity, signal location, or size of the signal of the detection agent. Sometimes, the profile or the detection profile may comprise about 100 frames, 500 frames, 1000 frames, 2000 frames, 5000 frames, 10,000 frames, 20,000 frames, 30,000 frames, 40,000 frames, 50,000 frames or more images. Analysis of the profile or the detection profile may determine the activity of the regulatory element. In some cases, the degree of activation may also be determined from the analysis of the profile or detection profile. In additional cases, analysis of the profile or the detection profile may further determine the optical isolation and localization of the detection agents, which may correlate to the localization of the regulatory element.

#### Detection of DNA and/or RNA Regulatory Elements

A regulatory element may be DNA. Described herein is a method of detecting a DNA regulatory element, which may include contacting a cell sample with a detection agent, binding the detection agent to the DNA regulatory element, and analyzing a profile from the detection agent to determine the presence, absence, or activity of the DNA regulatory element.

A regulatory element may be RNA. Described herein is a method of detecting a RNA regulatory element, which may include contacting a cell sample with a detection agent, binding the detection agent to the RNA regulatory element, and analyzing a profile from the detection agent to determine the presence, absence, or activity of the RNA regulatory element.

A regulatory element may be an enhancer RNA (eRNA). The presence of an eRNA may correlate to an activated regulatory element. For example, the production of an eRNA may correlate to the transcription of a target gene. As such, the detection of an eRNA element may indicate that a target gene downstream of the eRNA element may be activated.

Provided herein is a method of detecting an eRNA regulatory element, which may include contacting a cell sample with a detection agent, binding the detection agent to the eRNA regulatory element, and analyzing a profile from the detection agent to determine the presence, absence, or activity of the eRNA regulatory element. Described herein is an in situ method of detecting an activated regulatory DNA site, which may include incubating a sample with a set of detection agents (e.g., fluorescently-labeled probes), hybridizing the set of detection agents to at least one enhancer RNA (eRNA), and analyzing a profile (e.g., a fluorescent profile) from the set of detection agents to determine the presence of an eRNA, in which the presence of eRNA correlates to an activated regulatory DNA site.

Detection of a DNaseI Hypersensitive Site, Generation of a DNaseI Hypersensitive Site Map, and Determination of a Cell Type Based on a DNaseI Hypersensitive Site Profile

A regulatory element may be a DNaseI hypersensitive site (DHS). A DNaseI hypersensitive site may be an inactivated DNaseI hypersensitive site. A DNaseI hypersensitive site may be an activated DNaseI hypersensitive site. Described herein is a method of detecting a DHS, which may include contacting a cell sample with a detection agent, binding the detection agent to the DHS, and analyzing a profile from the detection agent to determine the presence, absence, or activity of the DHS.

The DHS may be an active DHS and may further contain a single stranded DNA region. The single stranded DNA region may be detected by S1 nuclease. A method of detecting a DHS may further be extended to detect the presence of a single stranded DNA region within a DHS. Such a method, for example, may comprise contacting a cell sample with a detection agent, binding the detection agent to a single stranded region of a DHS, and analyzing a profile from the detection agent to determine the presence or absence of the single stranded region within a DHS.

Also described herein is a method of determining the activity level of a regulatory element, which may include incubating a cell sample with a set of detection agents (e.g., fluorescently labeled probes), in which each detection agent hybridizes to a DHS, measuring a signature (e.g., a fluorescent signature) from the set of detection agents, and based on the signature, determining a DHS profile, and comparing the DHS profile with a control, in which a correlation with the control indicates the activity level of the regulatory element in the cell sample. The signature (e.g., the fluorescent signature) may further correlate to a signal intensity (or a peak height). A set of signal intensities may be compiled into a DHS profile and compared with a control to generate a second DHS profile which comprises a set of relative signal intensities (or relative peak heights). The set of relative signal intensities may correlate to the activity level of a regulatory element.

Also described herein is a method of generating a DHS map, which may provide information on cell-to-cell variation in gene expression, memory of early developmental fate decisions which establish lineage hierarchies, quantitation of embryonic stem cell DHS sites which decreases with cell passage, and presence of oncogenic elements.

The location of a set of DHS sites may be correlated to a cell type. For example, the location of about 1, about 5, about 10, about 15, about 20, about 25, about 30, about 35, about 40, about 45, about 50, about 55, about 60, or more DHS sites may be correlated to a cell type. The location of about 1, about 5, about 10, about 15, about 20, about 25, about 30, about 35, about 40, about 45, about 50, about 55, about 60, or more DHS may be used to determine a cell type. The cell may be a normal cell or a cancerous cell. DHS variation may be used to determine the presence of cancerous cells in a sample. A method of determining a cell type (e.g., a cancerous cell) may include incubating a cell sample with a set of detection agents (e.g., fluorescently labeled probes), in which each detection agent hybridizes to a DHS, measuring a signature (e.g., a fluorescent signature) from the set of detection agents, and based on the signature, determining a DHS profile, and comparing the DHS profile with a control, in which a correlation with the control indicates the cell type of the sample.

A DHS site may be visualized through a terminal deoxy-

nucleotidyl transferase (TdT) which may catalyze the addition of a dUTP at the site of a nick or strand break. A fluorescent moiety may further be conjugated to dUTP. A TUNEL assay may be utilized for visualization of a plurality of DHSs present in a cell. A TUNEL assay may be an assay as described in EXAMPLE 2.

The sequence of a DHS site may be detected in situ, by utilizing an in situ sequencing methodology. For example, the two ends of a padlock probe may be hybridized to a target regulatory element sequence and the two ends may be further ligated together by a ligase (e.g., T4 ligase) when bound to the target sequence. An amplification (e.g., a rolling circle amplification or RCA) may be performed utilizing a polymerase (e.g.,  $\Phi$ 29 polymerase), which may result in a single stranded DNA comprising at least about 1, at least about 2, at least about 3, at least about 4, at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, or more tandem copies of the target sequence. The amplified product at least about be sequenced by ligation in situ using partition sequencing compatible primers and labeled probes (e.g., fluorescently labeled probes). For example, each target sequence within the amplified product may bind to a primer and probe set resulting in a bright spot detectable by, e.g., an immunofluorescence microscopy. The labeled probe (e.g., the fluorescent label on the probe) may identify the nucleotide at the ligation site, thereby allowing the color detected to define the nucleotide at the respective ligation position. Sometimes, at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at 20, or more rounds of ligation and detection may, occur for detection of a DHS site.

A control as used herein may refer to a DHS profile generated from a regulatory element whose activity level is known. A control may also refer to a DHS profile generated from an inactivated regulatory element. A control may further refer to a DHS profile generated from an activated or inactivated regulatory element from a specific cell type. For example, the cell type may be an epithelial cell, connective tissue cell, muscle cell, or nerve cell type. The cell may be a cell derived from heart, lung, kidney, stomach, intestines, liver, pancreas, brain, esophagus, and the like. The cell type may be a hormone-secreting cell, such as a pituitary cell, a gut and respiratory tract cell, thyroid gland cell, adrenal gland cell, Leydig cell of testes, Theca interna cell of ovarian follicle, Juxtaglomerular cell, Macula densa cell, Peripolar cell, or Mesangial cell type. The cell may be a blood cell or a blood progenitor cell. The cell may be an immune system cell, e.g., monocytes, dendritic cell, neutrophil granulocyte, eosinophil granulocyte, basophil granulocyte, hybridoma cell, mast cell, helper T cell, suppressor T cell, cytotoxic T cell, Natural Killer T cell, B cell, or natural killer cell.

Detection and Mapping of a Chromatin

A regulatory element may also be a chromatin. Provided herein is a method of detecting a chromatin, which may include contacting a cell sample with a detection agent, binding the detection agent to the chromatin, and analyzing a profile from the detection agent to determine the activity state of the chromatin. The activity level of a chromatin may be determined based on the presence or activity level of a nucleic acid of interest or the presence or absence of a chromatin associated protein. The activity level of a chromatin may be determined based on DHS locations. The one or more DHS locations on a chromatin may be used to map chromatin activity state. For example, one or more DHSs may be localized in a region and the surrounding chromatin may be decompacted and readily visualized relative to an

inactive chromatin state when a DHS is not present. The one or more DHSs within a localized region may further form a localized DHS set and a plurality of localized DHS sets may further provide a global map or pattern of chromatin activity (e.g., an activity pattern).

Also included herein is a method of generating a chromatin map based on the pattern of DNaseI hypersensitive sites, RNA regulatory elements (e.g., eRNA), chromatin associated proteins or gene products, or a combination thereof. The method of generating a chromatin map may be based on the pattern of DNaseI hypersensitive sites. The method may comprise generating a 3-dimensional map from a detection profile (or a 2-dimensional detection profile). A chromatin map may provide information on the compaction of chromatin, the spatial structure, spacing of regulatory elements, and localization of the regulatory elements to globally map chromatin structure and accessibility.

A chromatin map for a cell type may also be generated, in which each cell type comprises a different chromatin pattern. Each cell type may be associated with at least one unique marker. The at least one unique marker (or fiduciary marker) may be a genomic sequence. The at least one unique marker (or fiduciary marker) may be DHS. A cell type may comprise about 5, about 10, about 15, about 20, about 25, about 30, about 35, about 40, about 45, about 50, about 60, or more unique markers (or fiduciary markers). The cell type may be an epithelia cell, a connective tissue cell, a muscle cell, a nerve cell, a hormone-secreting cell, a blood cell, an immune system cell, or a stem cell type. The cell type may be a cancerous cell type.

A chromatin profile (e.g., based on DHSs) in the presence of an exogenous agent or condition may also be generated. The method may comprise incubating a cell sample with a set of fluorescently labeled probes specific to target sites (e.g., target DHSs) on a chromatin in the presence of an exogenous agent or condition; measuring a fluorescent signature of the set of fluorescently labeled probes; based on the fluorescent signature, generating a fluorescent profile of the chromatin; and comparing the fluorescent profile with a second fluorescent profile of a chromatin obtained from an equivalent sample incubated with an equivalent set of fluorescently labeled probes in the absence of the exogenous agent or condition, wherein a difference between the two sets of fluorescent profiles indicates a change in the chromatin density (e.g., changes in the presences or activation of DHSs) induced by the exogenous agent or condition. The exogenous agent or condition may comprise a small molecule or a drug. The exogenous agent may be a small molecule, such as a steroid. The exogenous agent or condition may comprise an environmental factor, such as a change in pH, temperature, nutrient, or a combination thereof.

Methods of Determining the Localization of a Regulatory Element

Also described herein is a method for determining the localization of a regulatory element. The localization of a regulatory element may provide an activity state of the regulatory element. The localization of a regulatory element may also provide an interaction state with at least one additional regulatory element. For example, the localization of a first regulatory element with respect to a second regulatory element may provide spatial coordinate and distance information between the two regulatory elements, and v further provide information regarding whether the two regulatory elements may interact with each other. The activity state of a regulatory element may include, for example, a transcription or translation initiation event, a translocation event, or an interaction event with one or more additional

regulatory elements. The regulatory element may comprise DNA, RNA, polypeptides, or a combination thereof. The regulatory element may be DNA. The regulatory element may be RNA. The regulatory element may be an enhancer RNA (eRNA). The regulatory element may be a DNaseI hypersensitive site (DHS). The DHS may be an inactive DHS or an active DHS. The regulatory element may be a polypeptide. The regulatory element may be chromatin.

The localization of a regulatory element may include contacting a regulatory element with a first set of detection agents, photobleaching the first set of detection agents for a first time point at a first wavelength to generate a second set of detection agents capable of generating a light at a second wavelength, detecting at least one burst generated by the second set of detection agents to generate a detection profile of the second set of detection agents, and analyzing the detection profile to determine the localization of the regulatory element.

A detection agent may comprise a detectable moiety that is capable of generating a light, and a probe portion that is capable of hybridizing to a target site on a regulatory element. Each detection agent within the first set of detection agents may have the same or a different detectable moiety. Each detection agent within the first set of detection agents may have the same detectable moiety. A detectable moiety may comprise a small molecule (e.g., a fluorescent dye). A detectable moiety may comprise a fluorescently labeled polypeptide, a fluorescently labeled nucleic acid probe, and/or a fluorescently labeled polypeptide complex.

Upon photobleaching, a second set of detection agents may be generated from the first set of detection agents, in which the second set may include detection agents that are capable of generating a burst of light detectable at a second wavelength. For example, bleaching of the set of detection agents may lead to about 50%, about 60%, about 70%, about 80%, about 90%, or more detection agents within the set to enter into an "OFF-state". An "OFF-state" may be a dark state in which the detectable moiety crosses from the singlet excited or ON state to the triplet state or OFF-state in which detection of light (e.g., fluorescence) may be low (e.g., less than 10%, less than 5%, less than 1%, or less than 0.5% of the light may be detected). The remainder of the detection agents that have not entered into the OFF-state may generate bursts of lights, or to cycle between a singlet excited state (or ON-state) and a singlet ground state. As such, bleaching of the set of detection agents may generate about 40%, about 30%, about 20%, about 10%, about 5%, or less detection agents within the set that may generate bursts of lights. The bursts of lights may be detected stochastically, at a single burst level in which each burst of light correlates to a single detection agent.

A single wavelength may be used for photobleaching a set of detection agents. At least two wavelengths may be used for photobleaching a set of detection agents. A wavelength at 491 nm may be used. A wavelength at 405 nm may be used in combination with the wavelength at 491 nm. The two wavelengths may be applied simultaneously to photobleach a set of detection agents. Alternatively, the two wavelengths may be applied sequentially to photobleach a set of detection agents.

The time for photobleaching a set of detection agents may be from about 10 seconds to about 4 hours. The time may be from about 30 seconds to about 3.5 hours, from about one minute to about 3 hours, from about 5 minutes to about 2 hours, from about 10 minutes to about 1 hour, from about one minutes to about 1 hour, from about 5 minutes to about 1 hour, or from about 30 minutes to about 2 hours. The time

may be at least 10 seconds, at least 20 seconds, at least 30 seconds, at least 40 seconds, at least 50 seconds, at least 1 minute, at least 2 minutes, at least 3 minutes, at least 4 minutes, at least 5 minutes, at least 10 minutes, at least 15 minutes, at least 20 minutes, at least 30 minutes, at least 45 minutes, at least 1 hour, at least 1.5 hours, at least 2 hours, at least 2.5 hours, at least 3 hours, at least 3.5 hours, at least 4 hours, or more.

The concentration of the detection agents may be from about 5 nM to about 1  $\mu$ M. The concentration of the detection agent may be from about 5 nM to about 900 nM, from about 10 nM to about 800 nM, from about 15 nM to about 700 nM, from about 20 nM to about 500 nM, from about 10 nM to about 500 nM, from about 10 nM to about 400 nM, from about 10 nM to about 300 nM, from about 10 nM to about 200 nM, from about 10 nM to about 100 nM, from about 50 nM to about 500 nM, from about 50 nM to about 400 nM, from about 50 nM to about 300 nM, from about 50 nM to about 200 nM, from about 100 nM to about 500 nM, from about 100 nM to about 300 nM, or from about 100 nM to about 200 nM. The concentration of the detection agents may be about 10 nM, about 15 nM, about 20 nM, about 30 nM, about 40 nM, about 50 nM, about 60 nM, about 70 nM, about 80 nM, about 90 nM, about 100 nM, about 150 nM, about 200 nM, about 250 nM, about 300 nM, about 400 nM, about 500 nM, about 600 nM, about 700 nM, about 800 nM, about 900 nM, or more.

The burst of lights from the set of detection agents may generate a detection profile. The detection profile may comprise about 100 image frames, about 500 frames, about 1000 frames, about 2000 frames, about 5000 frames, about 10,000 frames, about 20,000 frames, about 30,000 frames, about 40,000 frames, about 50,000 frames, or more. The detection profile may also include the signal intensity, signal location, or size of the signal. Analysis of the detection profile may determine the optical isolation and localization of the detection agents, which may correlate to the localization of the regulatory element.

The detection profile may comprise a chromatic aberration correction. The detection profile may comprise less than 5%, less than 4%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.1%, or 0% chromatic aberration. The detection profile may comprise less than 5% chromatic aberration. The detection profile may comprise less than 4% chromatic aberration. The detection profile may comprise less than 3% chromatic aberration. The detection profile may comprise less than 2% chromatic aberration. The detection profile may comprise less than 1% chromatic aberration. The detection profile may comprise less than 0.5% chromatic aberration. The detection profile may comprise less than 0.1% chromatic aberration. The detection profile may comprise 0% chromatic aberration.

More than one regulatory element may be detected at the same time. At least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, or more regulatory elements may be detected at the same time. Each of the regulatory elements may be detected by a set of detection agents. The detectable moiety between the different set of detection agents may be the same. For example, two different sets of detection agents may be used to detect two different regulatory elements and the detectable moieties from the two sets of detection agents may be the same. As such, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, or more regulatory elements may be detected at the same time at the same wavelength. Sometimes, the detectable moiety between the different set of detection

agents may also be different. For example, two different sets of detection agents may be used to detect two different regulatory elements and the detectable moiety from one set of detection agents may be detected at a different wavelength from the detectable moiety of the second set of detection agents. As such, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, or more regulatory elements may be detected at the same time in which each of the regulatory elements may be detected at a different wavelength. The regulatory element may comprise DNA, RNA, polypeptides, or a combination thereof.

Methods of Measuring the Activity of a Regulatory Element

Also described herein is a method of measuring the activity of a target regulatory element. The method may include detection of a regulatory element and one or more products of the regulatory element. One or more products of the regulatory element may also include intermediate products or elements. The method may comprise contacting a cell sample with a first set and a second set of detection agents, in which the first set of detection agents interact with a target regulatory element within the cell and the second set of detection agents interact with at least one product of the target regulatory element, and analyzing a detection profile from the first set and the second set of detection agents, in which the presence or the absence of the at least one product indicates the activity of the target regulatory element.

As discussed herein, a detection agent may comprise a detectable moiety that is capable of generating a light, and a probe portion that is capable of hybridizing to a target site on a regulatory element. Each detection agent within the first set of detection agents may have the same or a different detectable moiety. Each detection agent within the first set of detection agents may have the same detectable moiety. A detectable moiety may comprise a small molecule (e.g., a fluorescent dye). A detectable moiety may comprise a fluorescently labeled polypeptide, a fluorescently labeled nucleic acid probe, and/or a fluorescently labeled polypeptide complex.

The method may also allow photobleaching of the first set and the second set of detection agents, thereby generating a subset of detection agents capable of generating a burst of light. A detection profile may be generated from the detection of a set of light bursts, in which the presence or the absence of the at least one product may indicate the activity of the target regulatory element.

The regulatory element may comprise DNA, RNA, polypeptides, or a combination thereof. The regulatory element may be DNA. The regulatory element may be RNA. The regulatory element may be an enhancer RNA (eRNA). The presence of an eRNA may correlate with target gene transcription that is downstream of eRNA. The regulatory element may be a DNaseI hypersensitive site (DHS). The DHS may be an activated DHS. The pattern of the DHS on a chromatin may correlate to the activity of the chromatin. The regulatory element may be a polypeptide, e.g., a transcription factor, a DNA or RNA-binding protein or binding fragment thereof, or a polypeptide that is involved in chemical modification. The regulatory element may be chromatin. Target Nucleic Acid Sequence

A target nucleic acid sequence may be a nucleic acid sequence of interest or may encode a DNA, RNA, or protein of interest or a portion thereof. A DNA, RNA, or protein of interest may be a DNA, RNA, or protein produced by a cell or contained within a cell. A target nucleic acid sequence may be incorporated into a structure of a cell. A target nucleic acid sequence may also be associated with a cell. For

example, a target nucleic acid sequence may be in contact with the exterior of a cell. A target nucleic acid sequence may be unassociated with a structure of a cell. For example, a target nucleic acid sequence may be a circulating nucleic acid sequence. A target nucleic acid sequence or a portion thereof may be artificially constructed or modified. A target nucleic acid sequence may be a natural biological product. A target nucleic acid sequence may be a short nucleic acid sequence. A target nucleic acid sequence may be a nucleic acid sequence that is from a source that is exogenous to a cell. A target nucleic acid sequence may be an endogenous nucleic acid sequence. A target nucleic acid sequence may be a nucleic acid sequence that comprises a combination of an endogenous nucleic acid sequence and a nucleic acid sequence from a source that is exogenous to a cell. A target nucleic acid sequence may be a chromosomal nucleic acid sequence or fragment thereof. A target nucleic acid sequence may be an episomal nucleic sequence or fragment thereof. A target nucleic acid sequence may be a sequence resulting from somatic rearrangement or somatic hypermutation, such as a nucleic acid sequence from a T cell receptor, B cell receptor, or fragment thereof.

A nucleic acid of a cell or sample, which may comprise the target nucleic acid sequence, may comprise a deoxyribonucleic acid (DNA) or a ribonucleic acid (RNA), or a combination thereof. A nucleic acid may be a chromosome, an oligonucleotide, a plasmid, an artificial chromosome, or a fragment or portion thereof. A nucleic acid may comprise genomic DNA, episomal DNA, complementary DNA, mitochondrial DNA, recombinant DNA, cell-free DNA (cfDNA), messenger RNA (mRNA), pre-mRNA, microRNA (miRNA), transfer RNA (tRNA), transfer messenger RNA (tmRNA), ribosomal RNA (rRNA), heterogeneous nuclear RNA (hnRNA), short interfering RNA (siRNA), anti-sense RNA, or short hairpin RNA (shRNA). A nucleic acid may be single-stranded, double-stranded, or a combination thereof.

A target nucleic acid sequence may comprise a naturally occurring nucleic acid sequence, an artificially constructed nucleic acid sequence (such as an artificially synthesized nucleic acid sequence), or a modified nucleic acid sequence (such as a naturally occurring nucleic acid sequence that has been altered or modified through a natural or artificial process).

A naturally occurring nucleic acid sequence may comprise a nucleic acid sequence present in a cellular sample. A naturally occurring nucleic acid sequence may comprise a nucleic acid sequence present in an unfixed cell. A naturally occurring nucleic acid sequence may comprise a nucleic acid sequence derived from a cellular sample.

A naturally occurring nucleic acid sequence may comprise a nucleic acid sequence present in an acellular sample. A naturally occurring nucleic acid sequence may comprise a nucleic acid sequence derived from an acellular sample. For example, a nucleic acid sequence may be a cell-free DNA sequence present in a bodily fluid (such as a sample of cerebrospinal fluid).

A nucleic acid may comprise a target nucleic acid sequence that is not endogenous to the source (exogenous) from which it was taken or in which it is analyzed.

A nucleic acid may be an artificially synthesized oligonucleotide.

A nucleic acid sequence may comprise one or more modifications. A modification may be a post-translational modification of a nucleic acid sequence or an epigenetic modification of nucleic acid sequence (e.g., modification to the methylation of a nucleic acid sequence). A modification

may be a genetic modification. A genetic modification to a nucleic acid sequence may be an insertion, a deletion, or a substitution of a nucleic acid sequence. A nucleic acid sequence modification may comprise an insertion may comprise transformation, transduction, or transfection of a sample. For example, a nucleic acid sequence modification comprising an insertion may result from infection or transduction of a cell with a virus and subsequent incorporation of a viral nucleic acid sequence into a nucleic acid sequence of the cells, such as the cell's genomic DNA. The integrated viral nucleic acid sequence (viral integrant) or fragment thereof may be the target nucleic acid sequence. Modification of a nucleic acid sequence may be an artificial modification, resulting from, for instance, genetic engineering or intentional nucleic acid sequence modification during nucleic acid fabrication. A nucleic acid sequence may be the result of somatic rearrangement.

A modification to a nucleic acid sequence comprising an insertion, deletion or substitution may comprise a difference between the nucleic acid sequence and a reference sequence. A reference sequence may be a nucleic acid sequence in a database, an artificial nucleic acid, a viral nucleic acid sequences, a nucleic acid sequence of the same cell, a nucleic acid sequence of a cell from the tissue, a nucleic acid sequence from a different tissue of the same subject, or a nucleic acid sequence from a subject of a different species.

A modification to a nucleic acid sequence may comprise a difference in 1 nucleotide (a single nucleotide polymorphism, SNP), at least 2 nucleotides, at least 3 nucleotides, at least 4 nucleotides, at least 5 nucleotides, at least 6 nucleotides, at least 7 nucleotides, at least 8 nucleotides, at least 9 nucleotides, at least 10 nucleotides, at least 25 nucleotides, at least 50 nucleotides, at least 100 nucleotides, at least 250 nucleotides, at least 500 nucleotides, at least 1,000 nucleotides, from 1 to 1,000 nucleotides, from 1 to 500 nucleotides, from 1 to 250 nucleotides, from 1 to 100 nucleotides, from 1 to 50 nucleotides, from 1 to 25 nucleotides, from 1 to 10 nucleotides, from 1 to 9 nucleotides, from 1 to 8 nucleotides, from 1 to 7 nucleotides, from 1 to 6 nucleotides, from 1 to 5 nucleotides, from 1 to 4 nucleotides, from 1 to 3 nucleotides, or from 1 to 2 nucleotides. Modification to a nucleic acid sequence comprising a difference in a plurality of nucleotides may comprise differences in two or more adjacent nucleotides or nucleotide sequences relative to a reference nucleic acid sequence. Modifications to a nucleic acid sequence comprising a difference in a plurality of nucleotides may also comprise differences in two or more non-adjacent nucleotides or nucleotide sequences (such as two or more modifications to the nucleic acid sequence that are separated by at least one nucleotide) relative to a reference nucleic acid sequence.

A target sequence may be assayed *in situ* or it may be isolated and/or purified from a cellular or acellular sample. For example, a target sequence comprising a nucleic acid may comprise a portion (a region) of genomic DNA located *in situ* in the nucleus of a fixed (intact) cell. A target sequence may comprise a nucleic acid sequence that is isolated from a sample (such as an aliquot of cerebrospinal fluid).

#### 60 Detection Agents

Detection agents may be utilized to detect nucleic acid sequence of interest. A detection agent may comprise a probe portion. The probe portion may include a probe, or a combination of probes. The probe portion may comprise a nucleic acid molecule, a polypeptide, or a combination thereof. The detection agents may further comprise a detectable moiety. The detectable moiety may comprise a fluoro-

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phore. A fluorophore may be a molecule that may absorb light at a first wavelength and transmit or emit light at a second wavelength. The fluorophore may be a small molecule (such as a dye) or a fluorescent polypeptide. The detectable moiety may be a fluorescent small molecule (such as a dye). The detectable moiety may not contain a fluorescent polypeptide. The detection agent may further comprise a conjugating moiety. The conjugating moiety may allow attachment of the detection agent to a nucleic acid sequence of interest. The detection agent may comprise a probe that is synthesized with direct dye incorporation at the 3' end.

FIG. 25 shows a schematic of a detection agent 100 for use with a Nano-FISH procedure. The detection agent may comprise a probe portion 110, as described herein. The detection agent may comprise a detectable moiety 120, as described herein.

## Probes

A detection agent may comprise a probe portion. A probe portion may comprise a probe or a combination of probes. A probe may be a nucleic acid probe, a polypeptide probe, or a combination thereof. A probe portion may be an unconjugated probe that does not contain a detectable moiety. A probe portion may be a conjugated probe which comprises a single probe with a detectable moiety, or two or more probes in which at least one probe may be an unconjugated probe bound to at least a second probe which comprises a detectable moiety.

A probe may be a nucleic acid probe. The nucleic acid probe may be a DNA probe, a RNA probe, or a combination thereof. The nucleic acid probe may be a DNA probe. The nucleic acid probe may be a RNA probe. The nucleic acid probe may be a double stranded nucleic acid probe, a single stranded nucleic acid probe, or may contain single-stranded and/or double stranded portions. The nucleic acid probe may further comprise overhangs on one or both termini, may further comprises blunt ends on one or both termini, or may further form a hairpin.

The nucleic acid probe may be at least 10, at least 15, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, at least 30,

## 30

at least 31, at least 32, at least 33, at least 34, at least 35, at least 36, at least 37, at least 38, at least 39, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 80, at least 90, at least 100, or more nucleotides in length. The nucleic acid probe may be about 10, about 15, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36, about 37, about 38, about 39, about 40, about 45, about 50, about 55, about 60, about 65, about 70, about 80, about 90, or about 100 nucleotides in length. The nucleic acid probe may be about 20 nucleotides in length. The nucleic acid probe may be about 21 nucleotides in length. The nucleic acid probe may be about 22 nucleotides in length. The nucleic acid probe may be about 23 nucleotides in length. The nucleic acid probe may be about 24 nucleotides in length. The nucleic acid probe may be about 25 nucleotides in length. The nucleic acid probe may be about 26 nucleotides in length. The nucleic acid probe may be about 27 nucleotides in length. The nucleic acid probe may be about 28 nucleotides in length. The nucleic acid probe may be about 29 nucleotides in length. The nucleic acid probe may be about 30 nucleotides in length. The nucleic acid probe may be about 31 nucleotides in length. The nucleic acid probe may be about 32 nucleotides in length. The nucleic acid probe may be about 33 nucleotides in length. The nucleic acid probe may be about 34 nucleotides in length. The nucleic acid probe may be about 35 nucleotides in length. The nucleic acid probe may be about 36 nucleotides in length. The nucleic acid probe may be about 37 nucleotides in length. The nucleic acid probe may be about 38 nucleotides in length. The nucleic acid probe may be about 39 nucleotides in length. The nucleic acid probe may be about 40 nucleotides in length. The nucleic acid probe may be about 45 nucleotides in length. The nucleic acid probe may be about 50 nucleotides in length. The nucleic acid probe may be about 55 nucleotides in length. The nucleic acid probe may be about 60 nucleotides in length.

TABLE 1 lists exemplary probe nucleotide sequences according to the present disclosure.

TABLE 1

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 1	TTTCCTTGCTCTTCATGATTTTAAACAACATGATGGATT
SEQ ID NO: 2	CCCTGCCCCCATTAACTCACATCCTGAATTTTATGTTTA
SEQ ID NO: 3	GCACCTTCATCATCGTCTTTGAAGTCCCCTTCTGTCTCC
SEQ ID NO: 4	TATGATGAACACCATGCACCACATGCAGGTTCTGGTGAAG
SEQ ID NO: 5	GATACAAAAGAATATTGGTATGTATGTTGCACAGACTCAT
SEQ ID NO: 6	CCTATTTCCCCCACACAGCCTTCCCACATGGCCAACCCCT
SEQ ID NO: 7	TACAAAGGGCTTCTCTGGCCAGAGAGAGCCGGTGTCTGCT
SEQ ID NO: 8	TGGGGGGTTAATGGAGTTATGGACTGGGATGGGCAGCCT
SEQ ID NO: 9	ACCTACCTAGGGAACCTTTCTCCCTGGCCACTAGGCTAGT
SEQ ID NO: 10	ACTGACTGAGCTGACCTCCAGTACAGGGCCCTGAGGCCACT
SEQ ID NO: 11	CTGGGAGCTAAATAGAAGCAAATATCCCCAGGCCCTGGGTG
SEQ ID NO: 12	ATGCGTCAAGCAACTACACTCCCACAGTAACTGGGAACC
SEQ ID NO: 13	CAGCTCCTTGGCAGCCTAGGCTCTAGCTCAACATCTGCTT

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 14	TGCTGGAGTCGCACCAACCTGGCTCTGCCTATCTCCAGCA
SEQ ID NO: 15	CTCTGTAGGCTGCACAACGTGGAACAGATGAAAGGAACCA
SEQ ID NO: 16	TGGGGTAAATTATAATCATGAAATCCGTCAAGCTTGAAT
SEQ ID NO: 17	AACATATTTAATATGGCATATTCAAATGACAGAAAAGTACG
SEQ ID NO: 18	CTTTATTCTTGCTAATGTTGACTCCTTAGCAAAGATAATT
SEQ ID NO: 19	TGATCTTTGCTAAACTCTTCAGGAATAAATGAACATTCC
SEQ ID NO: 20	TTTCAAGCAGTTAAGAAGCAAGAATTAATGACTCGAATA
SEQ ID NO: 21	ATGAGAGTGTGACTGATGAAGGGCTCCTATACGGGGTT
SEQ ID NO: 22	TCTTTCCCATCTGTTCCCGGCCCTACCAGAAATAAGTG
SEQ ID NO: 23	ATGAACCTCCCTCGCTCCAAGACCAGAGCTCCTAGGAAGT
SEQ ID NO: 24	TCTTTATTTTATTGGCCACAATTGAACATAGGTATAATTT
SEQ ID NO: 25	CAGAAGCAAGCCCTGATCAAGGAAACCATTCACTTGAT
SEQ ID NO: 26	GTGGCTTTTGCTCAAAGTGAGGACGTTATCAGCTCTGCC
SEQ ID NO: 27	CTTTAAACAAAACATAAAGCGTAAGGAAAGATAACTACT
SEQ ID NO: 28	CAGTTGCCACACTTTTTTCACTGCTAAAGTTCGTAATGA
SEQ ID NO: 29	GGCAATCAGAAGTATTTGGTTGCTCTAGGTCAGAATGA
SEQ ID NO: 30	GGCAGCAAACCTGTTTAGGTATGATTCATCATTGCTCTGCT
SEQ ID NO: 31	CTACAAAACAATGAGTCTGATTACGACCCACAGAAATGAA
SEQ ID NO: 32	CCTCCACAGACCCAAACATGCTGCTGCAAATGTCTCACT
SEQ ID NO: 33	GGACAAGCACACACATCGCTGGGAGATCTGCAAGCCTCC
SEQ ID NO: 34	TAAACCTGGATAACAAGAACACTGTTTCCACTGCGCTAGT
SEQ ID NO: 35	TCATCACGATGACAATGGACAAGCCATATCCCTAACAGGG
SEQ ID NO: 36	TTTCCATGACACCAGGACCGTAAAGCACCTTTTACACCGT
SEQ ID NO: 37	AATTGGGATGTGCAAAACCTCTTAACTGTAGCACCAAGT
SEQ ID NO: 38	TCTTGTTTATTTCGCTGCATTGAAATCCCATCCCAATCC
SEQ ID NO: 39	TGAGTGATCTCTTTGCTGATCATAAACATATTCCTCCATC
SEQ ID NO: 40	TGCATTCACTACTAAATACACAGGGCATAGCACATAGTAA
SEQ ID NO: 41	CTTCAATGTTGCCAGGAAAATCCTTGCAAGGAATCACACCC
SEQ ID NO: 42	ATTTTTTCTAAAGCTTTAGGAAATACACACGTTTCCCT
SEQ ID NO: 43	AGAGTAATCTTCAACAATCCTTGGTCTAAACACACACAAG
SEQ ID NO: 44	CCCAGGGACCCACGCCAAGCTCACCGCACCTTCCACCAA
SEQ ID NO: 45	AGCTCCTGTACTAGCTGGTGGGGTGTGGAGCACACAGCCC
SEQ ID NO: 46	TCACACAGGGAAAGTGAGGCTTGGTGGTTGATTTGAGCAA
SEQ ID NO: 47	CCTTCCAACAGCCGTGTGAGACAAGAGTCTTATCCTCTT
SEQ ID NO: 48	ACAAGGGTCACTGAGCACATGCCATGTGTGGGCACAGTG
SEQ ID NO: 49	GTCTCCTAAGTCTCATTCTTTCTTAGGATCTTCAGATC
SEQ ID NO: 50	TCCGCCTAAGTAAAACATAAAATTAAGCTGCGTAAA
SEQ ID NO: 51	CATTTTGACCTGATTATCTTTGTCTATAAGCTTAAGCCA

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 52	CCGGTTCCTCCACCCTCACTGCCCCAACAACTGAAAGAAG
SEQ ID NO: 53	ACAGTGTGTTGAAAGAATCCATAACTCTTTCTTTCCAGCC
SEQ ID NO: 54	GAAGTTTCATCTTTATCAAATCTCCATTCCCAGGCGGAC
SEQ ID NO: 55	AAGTCCATTTTTTTAAGCTTTGCGCTTCAGCTCCAGAACA
SEQ ID NO: 56	TCTTCGTTATGAATACAATAGGAAAACAATCAGACCCAA
SEQ ID NO: 57	TCCTCGGGGCATTCTAGAACCCTAGCAGACCTGCTTACAT
SEQ ID NO: 58	TCCTTATGTGGGAAAATAAGAGGATAGACAGATTTGATT
SEQ ID NO: 59	AGCTGCGAGTCCCTAACAGACTTCCAGGACAGCTGAAAA
SEQ ID NO: 60	AGGACAAGGGAGAGACGCCACCCGCCCTCTGTCAGGGATA
SEQ ID NO: 61	AATCCATGAGGGTGACATACACATCCTTACTGTTCCACA
SEQ ID NO: 62	ACTTCCTTCCCTGAGATGCCCATCCTTTGATTCTGGGATT
SEQ ID NO: 63	GCTCCCGGATAAATAATTACCGTGACCCTGAGCTGCTTC
SEQ ID NO: 64	TAGACTAAGAGAATCTAATTTGTGGCAAAGATCTTGAGTG
SEQ ID NO: 65	TGAAGGATGACTAAGAGCTTCCCTATAAACCCCATACTGG
SEQ ID NO: 66	AGCCAGGACTATAGAGTTTCAGAAAAGGGAGAAAATTCTA
SEQ ID NO: 67	TGCTGCTAATTTAAGTTTCTGGCAAGTCAAATAAATCTC
SEQ ID NO: 68	CGAAAACCATCAATTAAGTGAATGATCAGGAAATTGCGT
SEQ ID NO: 69	TTTATTTAGTCCCAGGGTGTATGAAGTGCTTCCAGGC
SEQ ID NO: 70	GGTCCTTCTTGGTACCGATATTGCCATATTGGCTGGACAT
SEQ ID NO: 71	TGGCTTGGTAGGATGCACTCACATGGGCTGTAGTAATACT
SEQ ID NO: 72	TATCACCAGCATAACTTGTGGTTCTTCAGCCAGTAATTC
SEQ ID NO: 73	GAACAAC TGGGATCTACAGGCAAAGAAATGAACCTTGAC
SEQ ID NO: 74	TAGGTAAGTGTGTCCCTATATATTTGACTTGGTAATAA
SEQ ID NO: 75	TATGTGAACATCGGTGAATATCATAATTTATTATGCAAAC
SEQ ID NO: 76	AGCTGAACACTCTTTGTGGTCTCTTGAAGCCTAGAATTA
SEQ ID NO: 77	CCCCACCTCACTGCCCCCAGTTCTGACTCAGGGTGTCCC
SEQ ID NO: 78	ACTCCCATCACCTGGCCAGCTTGGCTGTCCCTGACCCAC
SEQ ID NO: 79	GGCTGCCAGCTGCCAGCAGCAAAC TGCATAGGAAC T C
SEQ ID NO: 80	GCCCAGGACGCCAAGTGTCAACCCCTCTCCCCAGGCAGG
SEQ ID NO: 81	CACAAGGTCAGCTCCACCCGTGGGTGAGTGTGCCCCAGAT
SEQ ID NO: 82	GGAGACAAAACGGGCACCCAGCCAGTCATGCCGTGCCT
SEQ ID NO: 83	CTGAAATCAGTCAGCAGTTTCGGTGAGTCTGCAGTGACA
SEQ ID NO: 84	CGCCACATTTGGGGCTGGGAGAGATGTCACAGGGGCTGAC
SEQ ID NO: 85	CACATGTTCTCTGCATAGGTTTTTAAGCAGCCAGCAGCTG
SEQ ID NO: 86	TTTAAATGAAAACCCACACTTCCAAAATAGCACTTGAGT
SEQ ID NO: 87	AACATGTTTGTGTAATTAAGCATTTTAAATCATAACCAT
SEQ ID NO: 88	TGCTTATCTGTGCTTTTTATGTTCCACCCCCCACCACCA
SEQ ID NO: 89	ATTAATAATAATTCTGTGTTTATGGGGATTGCAGATACAT

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 90	CCAGCTTTGTGTCTTCATGACCCAACTGGAGTAAGAATGG
SEQ ID NO: 91	AAAGACCTCATTTCAGCATGGTTAGCAGTGTCAAACATT
SEQ ID NO: 92	TCTCGTAGCACTGGCTGCAGCCGGCCTGTGTGCCCCACC
SEQ ID NO: 93	GCCTTCATCCTGAACGGCTGACCAGCGGAAACAAAAGATC
SEQ ID NO: 94	ATGGCCAGATAACAGTGTTTAGACATGTCTTTGATGTTTT
SEQ ID NO: 95	CCCTGACTGTGTAAGGGTCTCTCTCCATGGGGAATAGAG
SEQ ID NO: 96	CTGAGCTTAGCTTCTACTGTGCTGTTAATTTAGGCAAGA
SEQ ID NO: 97	AGATCAATAATATTGCATTAGCTACTTACATCAGTCTCT
SEQ ID NO: 98	TAATTGCAGAAAACCTATAAAGCATGGAAGAATACAAAAC
SEQ ID NO: 99	AAACAAATTCCTCTACCTGGACATGACTGTTGTTAGCATT
SEQ ID NO: 100	GGGAGATTCTTCATATCCTTTTAAATGTAGATATGCACATT
SEQ ID NO: 101	ACAAAAAAGGCTATCATATTGTACATATAACTTTGCTGTA
SEQ ID NO: 102	TCTGCTAGGAACCTGTACCCATGTCATTACTGTAAGCATT
SEQ ID NO: 103	ACTACTCAAATTTTAGTATCTGCAGATATCAGATATCCTT
SEQ ID NO: 104	TGAAATGGTATTGTTGCCCTTTCTGATTAGTAAAGTATAC
SEQ ID NO: 105	TTATAATCTAGCAAGGTTAGAGATCATGGATCACTTTCAG
SEQ ID NO: 106	ACAGCTTGCCTCCGATAAGCCAGAATCCAGAGCTTCTGG
SEQ ID NO: 107	TCAATCAACCTGATAGCTTAGGGGATAAACTAATTTGAAG
SEQ ID NO: 108	GATCATGAAGGATGAAAGAATTCACCAATATTATAATAA
SEQ ID NO: 109	TTTAGCCATCTGTATCAATGAGCAGATATAAGCTTTACAC
SEQ ID NO: 110	AGGGGTAGATTATTTATGCTGCCATTTTGTAGCCATAAA
SEQ ID NO: 111	CACTACCATTTACAATTCGCACTTCTTTCTTTGTCCTT
SEQ ID NO: 112	GCTCCATCAAATCATAAAGGACCCACTTCAAATGCCATCA
SEQ ID NO: 113	TCCTACTTTCAGGAACTTCTTTCTCCAAACGTCTTCTGCC
SEQ ID NO: 114	AATTCATTTTTTCTTCAACGTACTTTAGGCTTGTAAATGT
SEQ ID NO: 115	TAAGATGCAAATAGTAAGCCTGAGCCCTTCTGTCTAACTT
SEQ ID NO: 116	CTGTGTTTCAGAATAAAATACCAACTCTACTACTCTCATC
SEQ ID NO: 117	GAAACCATGTTTATCTCAGGTTTACAAATCTCCACTTGTC
SEQ ID NO: 118	CTTTGAAAAGTAATCAGGTTTAGAGGAGCTCATGAGAGC
SEQ ID NO: 119	GCTGAATCCCAACTCCAATTGGCTCCATTTGTGGGGGA
SEQ ID NO: 120	GGTGTATGAACTTAACGCTTGTGTCTCCAGAAAATTCAC
SEQ ID NO: 121	AGTTAATGCACGTTAATAAGCAAGAGTTAGTTTAAATGTG
SEQ ID NO: 122	TAATTGAGAAGGCAGATTCAGTGGAGTTCTTATATAATTG
SEQ ID NO: 123	CACGGTCAGATGAAAATATAGTGTGAAGAATTTGTATAAC
SEQ ID NO: 124	CACAAGTCAGCATCAGCGTGTATGTCTCAGCAGCAGAAC
SEQ ID NO: 125	GGAGGTGGGGACTTAGGTGAAGGAAATGAGCCAGCAGAAG
SEQ ID NO: 126	GTCACAGCATTTCAAGGAGGAGACCTCATTGTAAGCTTCT
SEQ ID NO: 127	AAAGAGGTGAAATTAATCCCATACCTTAAGTCTACAGAC

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 128	CTTTACTAAGGAACCTTTTCATTTTAAGTGTGACGCATGC
SEQ ID NO: 129	CAGGTTTTTCTTTCCACGGTAAC TACAATGAAGTATCCT
SEQ ID NO: 130	GCTCTACAGGAGGTTGAGGTGTAGAGATCAGAGCAGGA
SEQ ID NO: 131	TACTATTTCCAACGGCATCTGGCTTTTCTCAGCCCTTGTG
SEQ ID NO: 132	AAGGTTTAGGCAGGATAGCCATTCTATTTTATTAGGGGC
SEQ ID NO: 133	AGGGGCTCAACGAAGAAAAAGTGTCCAAGCTTTAGGAAG
SEQ ID NO: 134	GGGCTGAACCCCTTCCCTGGATTGCAGCACAGCAGCGAG
SEQ ID NO: 135	CTGACGTCATAATCTACCAAGTCATGGATCGAGTTCAGA
SEQ ID NO: 136	GAAGGTAGAGCTCTCCTCCAATAAGCCAGATTTCCAGAGT
SEQ ID NO: 137	CACCAATATTATTATAATTCCTATCAACCTGATAGGTTAG
SEQ ID NO: 138	AGATATAAGCCTTACACAGGATTATGAAGTCTGAAAGGAT
SEQ ID NO: 139	ACATGTATCTTTCTGGTCTTTTAGCCGCTAACACTTGA
SEQ ID NO: 140	CAAAGAACAAGTGCAATATGTGCAGCTTGTGTGCGCAGGT
SEQ ID NO: 141	TATTATTATGTGAGTAAGTGAAGATACTGATAAGTTGAC
SEQ ID NO: 142	TAAAAATCTTTCTCACCCATCCTTAGATTGAGAGAAGTCA
SEQ ID NO: 143	TGGGTTTACCTCAGTCTCTATAATCTGTACCAGCATAACC
SEQ ID NO: 144	CACACCCATCTCACAGATCCCTATCTTAAAGAGACCCTA
SEQ ID NO: 145	ATGGAACCAACAGACTCTCAGATATGGCCAAAGATCTA
SEQ ID NO: 146	GACACCAGTCTCTGACACATTCTTAAAGGTCAGGCTCTAC
SEQ ID NO: 147	AGAGATCAAAGATTCACTTGTTTAGGCCTTAGCGGGCT
SEQ ID NO: 148	TCCTTAGTCTGAGGAGGCAATTAAGATTCACTTGTTTA
SEQ ID NO: 149	TAAATGGGAAGTTGTTTGAACAGGAGGATCCTAGAT
SEQ ID NO: 150	GGGTTTATACATGACTTTTAGAACACTGCCTTGGTTTTTG
SEQ ID NO: 151	AACTCTTAAAAGATATTGCCTCAAAGCATAAGAGGAAAT
SEQ ID NO: 152	AAATCGAGGAATAAGACAGTTATGGATAAGGAGAAATCAA
SEQ ID NO: 153	TCAGTTAGGATTTAATCAATGTCAGAAGCAATGATATAGG
SEQ ID NO: 154	CTTGAAAACACTTGAAATTGCTTGTGTAAAGAAACAGTTT
SEQ ID NO: 155	ATAATCTTCAGAGGAAAGTTTTATTCTCTGACTTATTTAA
SEQ ID NO: 156	AGATTCCTTCTGTCAATTTTGCCTCTGTTTCAATACTTCT
SEQ ID NO: 157	ATTTACAGCTTCTAAACTTTATTTGGCAATGCCTTCCCATG
SEQ ID NO: 158	GCAGGAGTTTGTCTTCTCTGCTTCAGAGCTTTGAATTTA
SEQ ID NO: 159	ACATATCAACGGCACTGGTCTTTATCTAACTCTCTGGCA
SEQ ID NO: 160	TTATGCTTCCCTGAAACAATACCACCTGCTATTCTCCACT
SEQ ID NO: 161	TTCTCACTCCCTACCCTGAGGACAAGTTTATGTCCTTAG
SEQ ID NO: 162	TTAGAGATTATGTCATTACCAGAGTTAAAATCTATAATG
SEQ ID NO: 163	GGTCATTCTTAGAATAGTAATCCAGCCAATAGTACAGGTT
SEQ ID NO: 164	CAGGCAATAAGGGCTTTTAAAGCAAAACAGTTGTGATAAA
SEQ ID NO: 165	ATGATGGGCACTGAAGGTTAAAACCTTGAGTCTGTCACTT

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 166	AACTCATAAATATCCCATTTTCCGCTGAAATATAGCTTTA
SEQ ID NO: 167	CCTGGTTTCTTTGACCTTTTGGGACCTTGAGTAAGTAAAG
SEQ ID NO: 168	CTTCATTATTTTCATGATTAATAATCTAAGAAATCTTG
SEQ ID NO: 169	TTTTAATTAATTCATGCTAATGTATTTATGAACTA
SEQ ID NO: 170	CATAGAAATAAACAATACTCTGAAGTAGTTCAGAATGTG
SEQ ID NO: 171	CAATTTATATAAAGAGTTAATTCAAATGAGACTATTTTAA
SEQ ID NO: 172	AGGGCTTTGAATCTTATGTCTAGAAATTTGAAAAACCTC
SEQ ID NO: 173	TATATGCTAAGATCCACCTCTAGTGTAGAACTGAGAAG
SEQ ID NO: 174	TGACTTGGTGATCTTTTAAATCTGAAACAACAGCAAC
SEQ ID NO: 175	AGCTAAGGACTTTTCTTGCCATGCTATGCTATCTTCAGT
SEQ ID NO: 176	TGATTATTTAGTATGAAACTATAACATAGTATGTTTCCT
SEQ ID NO: 177	AAAAAATGTGTATTTCTCTGGAGAAGTTAAAACTGAGGA
SEQ ID NO: 178	CAAGTGAGCAAGGCTTAAATGGAAGAAGCAATGATCTCGT
SEQ ID NO: 179	CCACCTTCATTAACGAGATCATCCATCATGAGGAAATATG
SEQ ID NO: 180	ACCAGGCCCCCTCTGTTTTGTGTCACTAAGGGTGGAGATG
SEQ ID NO: 181	ATGATTTTTCCCTCCCCGGGCTTCTTTAGCCATCAATA
SEQ ID NO: 182	TAGCCCCACAGGAGTTTGTCTGAAAGTAAACTCCACAA
SEQ ID NO: 183	AAGCTTATTGAGGCTAAGGCATCTGTGAAGGAAAGAAACA
SEQ ID NO: 184	CTCTAAACCACTATGCTGCTAGAGCCTCTTTCTGTACTC
SEQ ID NO: 185	CTCATTGAGACTAGTGTACCAGTCTCCTCATATACCT
SEQ ID NO: 186	TATTTTCTTCTTCTGTGTTTAGTCATGTTTCTGGGA
SEQ ID NO: 187	GGCAAACCCATTATTTTTTCTTTAGACTTGGGATGGTGA
SEQ ID NO: 188	TGGGCAGCGTCAGAACTGTGTGTGGATATAGATAAGAGC
SEQ ID NO: 189	GACTATGCTGAGCTGTGATGAGGGAGGGCCTAGCTAAAG
SEQ ID NO: 190	TGAGAGTCAGAAATGCTCCTGCTATTGCCTTCTCAGTCCCC
SEQ ID NO: 191	TTGGTTTCTACACAAGTAGATACATAGAAAAGGCTATAGG
SEQ ID NO: 192	TGTTTGAGAGTCCTGCATGATTAGTTGCTCAGAAATGCC
SEQ ID NO: 193	TTACAAATATGTGATTATCATCAAACGTGAGGGCTAAAG
SEQ ID NO: 194	CAGATAACTTGCAAGTCCTAGGATACCAGGAAAATAAATT
SEQ ID NO: 195	AGCATTATGTCTGTCTGTCATGTTTTTCATCCTCTTGTA
SEQ ID NO: 196	TTCACAGTTACCCACACAGGTGAACCCCTTTAGCTCTCCT
SEQ ID NO: 197	GAATGTTTCTTCTCTCAGGATCAGAGTTGCCTACATCT
SEQ ID NO: 198	AATGCACCAAGACTGGCCTGAGATGTATCCTTAAGATGAG
SEQ ID NO: 199	TCCCAGTAGCACCCCAAGTCAGATCTGACCCCGTATGTGA
SEQ ID NO: 200	GTGTCCTCTAACAGCACAGGCCTTTGCCACCTAGCTGTC
SEQ ID NO: 201	GGCAAACAAGGTTTGTCTTTCTTTCTGTTTTTCATGCCTT
SEQ ID NO: 202	TTCCATATCCTTGTTCATATTAATACATGTGTATAGATC
SEQ ID NO: 203	AAATCTATACACATGTATTAATAAAGCCTGATTCTGCCGC

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 204	AGGTATAGAGGCCACCTGCAAGATAAAATATTTGATTACACA
SEQ ID NO: 205	CTAATCATTCTATGGCAATTGATAACAACAATATATATA
SEQ ID NO: 206	ATAATATATTCTAGAATATGTCACATTCTGTCTCAGGCAT
SEQ ID NO: 207	TTTCTTTATGATGCCGTTTGAGGTGGAGTTTTAGTCAGGT
SEQ ID NO: 208	AGCTTCTCCTTTTTTTTGCCATCTGCCCTGTAAGCATCCT
SEQ ID NO: 209	GGGACCCAGATAGGAGTCATCACTCTAGGCTGAGAACATC
SEQ ID NO: 210	CACACACCCTAAGCCTCAGCATGACTCATCATGACTCAGC
SEQ ID NO: 211	CTGTGCTTGAGCCAGAAGGTTTGCTTAGAAGGTTACACAG
SEQ ID NO: 212	AACTGCTCATGCTTGACTATGGGAGGTCATAATGGAGA
SEQ ID NO: 213	CAGAAATGTAACAGGAAC TAAGGAAAACTGAAGCTTATT
SEQ ID NO: 214	CAGAGATGAGGATGCTGGAAGGGATAGAGGGAGCTGAGCT
SEQ ID NO: 215	AAAAGTATAGTAATCATTCAGCAAATGGTTTTGAAGCAC
SEQ ID NO: 216	GTATCTTATTTCCCAAGAGTCCAAGTAAAAATAACAG
SEQ ID NO: 217	GAAAAGAATGTTTCTCTCACTGTGGATTATTTAGAGAGT
SEQ ID NO: 218	AATGGTCAAGATTTTTTAAAAAATAAGAAAACATAAGTT
SEQ ID NO: 219	CTTGAGAAATGAAAAATTTATTTTTTTGTTGGAGGATACCC
SEQ ID NO: 220	TCTATCTCCCATCAGGGCAAGCTGTAAGGAACTGGCTAAG
SEQ ID NO: 221	AGTGAGACAGAGTACTTAGTCTTAGAGGCCCACTGGTA
SEQ ID NO: 222	GATGAGAAGGCACCTTCATCACTCATCACAGTCAGCTCTG
SEQ ID NO: 223	TCTCCTCTCTCCTTCTCATCAGAAATTCATAAGTCTAC
SEQ ID NO: 224	GTCAGGCAGATCACATAAGAAAAGAGGATGCCAGTTAAGG
SEQ ID NO: 225	GTTGCTGTTAGACAATTTTATCTGTGCCCTGCTTAGGAGC
SEQ ID NO: 226	TCTTTAATGAAAGCTAAGCTTTCATTAAAAAAAGTCTAAC
SEQ ID NO: 227	TGCATTGCACTTTGACTGCAGCAGCTGGTTAGAAGGTCT
SEQ ID NO: 228	GAGGAGGGTCCCAGCCATTGCTAAATTAACATCAGGCTC
SEQ ID NO: 229	ACTGGCAGTATATCTCTAACAGTGGTTGATGCTATCTTCT
SEQ ID NO: 230	CTTGCTGCTACATTGAGACCACTGACCCATACATAGGAA
SEQ ID NO: 231	ATAGCTCTGTCTGAACTGTTAGGCCACTGGTCCAGAGAG
SEQ ID NO: 232	CATCTCCTTTGATCCTCATAATAACCTATGAGATAGACA
SEQ ID NO: 233	TATTACTCTTACTTTATAGATGATGATCCTGAAAAATAG
SEQ ID NO: 234	CAAGGCACTTGCCCTTAGCTGGGGTATAGGGGAGCAGTC
SEQ ID NO: 235	GTAGTAGTAGAATGAAAAATGCTGCTATGCTGTGCCCTCCC
SEQ ID NO: 236	CTTTCCCATGCTGCCCTCTACTCATGGTCTATCTCTCCT
SEQ ID NO: 237	CCTGGGAGTCATGGACTCCACCCAGCACCACCAACCTGAC
SEQ ID NO: 238	CCACCTATCTGAGCCTGCCAGCCTATAACCCATCTGGGCC
SEQ ID NO: 239	TAGCTGGTGGCCAGCCCTGACCCACCCACCCCTCCCTGG
SEQ ID NO: 240	TCTGATAGACACATCTGGCACACCAGCTCGCAAAGTCACC
SEQ ID NO: 241	GGGTCTGTGTTTGCTGAGTCAAATTCCTTGAATCCAA

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 242	TTAGAGACTCCTGCTCCCAAATTTACAGTCATAGACTTCT
SEQ ID NO: 243	GGCTGTCTCCTTTATCCACAGAATGATTCCTTTGCTTCAT
SEQ ID NO: 244	CCATCCATCTGATCCTCCTCATCAGTGACGACAGGGCCC
SEQ ID NO: 245	GCAGTAGCTGCAGAGTCTCACATAGGTCTGGCACTGCCTC
SEQ ID NO: 246	ATGTCCGACCTTAGGCAAATGCTTGACTCTTCTGAGCTCA
SEQ ID NO: 247	TGTCATGGCAAAATAAAGATAATAATAGTGTTTTTTATG
SEQ ID NO: 248	TAGCGTGAGGATGGAAAAAATAGCAAAATGATTAGACT
SEQ ID NO: 249	AAGGTCTCAACAAATAGTAGTAGATTTTATCGTCCATTAA
SEQ ID NO: 250	TCCCTCTCCTCTTACTCATCCCATCACGTATGCCTCTT
SEQ ID NO: 251	TCCCTTACCTATAATAAGAGTTATTCCTCTTATTATATT
SEQ ID NO: 252	TTATAGTGATTTGGATATTTAAAGTGGGAATGAGGGGCGAG
SEQ ID NO: 253	CTAACGAAGAAGATGTTTCTCAAAGAAGCCATTCTCCCCA
SEQ ID NO: 254	GATCATCTCAGCAGGGTTCAGGAAGATAAAGGAGGATCAA
SEQ ID NO: 255	TGTTGAGGTGGGAGGACCGCTTGAGCCTGGGAAGTGCAAG
SEQ ID NO: 256	AGTGAGCCGAGATTTTGCCACTACACTCCCATTGGGTGA
SEQ ID NO: 257	GTGAGACCCTTTCTCAAAAACAACTAATTA AAAAACCCCT
SEQ ID NO: 258	TTTACAGATGAAGAACTGAGTCATACA ACTACTAAGAGA
SEQ ID NO: 259	GAGTCACTAATCACTCAGGTGGTCTGGCTCCAGCATCTGT
SEQ ID NO: 260	TTAATCTCTGCTCTATACTGCCCAAGACTTTTATAAAGTC
SEQ ID NO: 261	GTTGAGTCACTGAAATGAGTTATTGGGATGGCTGTGTGGG
SEQ ID NO: 262	GTGCTAAGTTCTTTCTAAAGGTATGTGAGAATACAAAGG
SEQ ID NO: 263	AAGCATCCTCCTTTTACACACGTGAACTAGTGATGCAA
SEQ ID NO: 264	GACACTCAGTGGCCTGGGTGAAGTGAGAATTTTATTGC
SEQ ID NO: 265	TGAGAGCCTCTGGGACATCTTGCCAGTCAATGAGTCTCA
SEQ ID NO: 266	CAATTCCTTCTCAGTCTTGAGTAACAGAAGCTCATGCA
SEQ ID NO: 267	ATAAACGGAAATTTGTATTGAAATGAGAGCCATGGA
SEQ ID NO: 268	TTACTCCAGACTCCTACTTATAAAAAGAGAACTGAGGCT
SEQ ID NO: 269	GAAGGTGGGGACTTTCTCAGTATGACATGGAAATGATCA
SEQ ID NO: 270	TGGATTCAAAGCTCCTGACTTCTGTCTAGTGTATGTGCA
SEQ ID NO: 271	GCCCTTTTCCTCTAACTGAAAGAAGGAAAAAAAAATGGA
SEQ ID NO: 272	AAAATATTCTACATAGTTTCCATGTCACAGCCAGGGCTGG
SEQ ID NO: 273	TCTCCTGTTATTTCTTTTAAAATAAATATATCATTTAAAT
SEQ ID NO: 274	AAATAAGCAAACCTGCTCGGGAATGGGAGGAGAGTCTC
SEQ ID NO: 275	GTCCACCCCTTCTCGGCCCTGGCTCTGCAGATAGTGTAT
SEQ ID NO: 276	GCCCTGACAGAGCCCTGCCATTGCTGGGCCTTGGAGTGA
SEQ ID NO: 277	GCCTAGTAGAGAGGCAAGCCATCTCATAGCTGCTG
SEQ ID NO: 278	GGAGAGAGAAAAGGGCTCATTGTCTATAAACTCAGGTCAT
SEQ ID NO: 279	ATTCTTATTCTCACACTAAGAAAAAGAATGAGATGTCTAC

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 280	ACCCTGCGTCCCCTCTTGTGTACTGGGGTCCCCAAGAGCT
SEQ ID NO: 281	AAAAGTGATGGCAAAGTCATTGCGCTAGATGCCATCCCAT
SEQ ID NO: 282	TATAAACCTGCATTGTCTCCACACACCAGTCATGGACAA
SEQ ID NO: 283	CCTCCTCCCAGGTCCACGTGCTTGTCTTTGTATAATACTC
SEQ ID NO: 284	AATTTCCGAAAATGTATTCTTTCAATCTTGTCTGTTATT
SEQ ID NO: 285	TTTCAATGGCTTAGTAGAAAAAGTACATACTTGTTTTCCC
SEQ ID NO: 286	ATTGACAATAGACAATTTACATCAATGTCTATATGGGTC
SEQ ID NO: 287	TGTTTGCTGTGTTTGCAAAAACACATAAATTATATT
SEQ ID NO: 288	CTACTCTAAGAAAGTTACAACATGGTGAATACAAGAGAAA
SEQ ID NO: 289	TTACAAGTCCAGAAAATAAAAGTTATCATCTTGAGGCCTC
SEQ ID NO: 290	TTCTAGGAATAATATCAATATTACAAAATTAATCTAACAA
SEQ ID NO: 291	GAACAGCAATGAGATAATGTGTACAAAGTACCCAGACCTA
SEQ ID NO: 292	GTAGAGCATCAAGGAAGCGCATTGCGGAGCAGTTTTTGT
SEQ ID NO: 293	TTGTTTTTGTATTCTGTTTCGTGAGGCAAGGTTTCACTCT
SEQ ID NO: 294	TCCAGGCTGGAGTGCAAGTGCAGATCATGTCTCACTGCA
SEQ ID NO: 295	TGACCTCCTGAGCTCAAGGGATCCTCCATTTCCGGCCTCC
SEQ ID NO: 296	TAGCTGGGACTACAGGTGTACATCACATGCCTGGCTAATT
SEQ ID NO: 297	TTTTTTTTTAAGTAGAGACGAGGCTTGCTATGTTGTCC
SEQ ID NO: 298	TAATATCAAACCTCTTGAGCTCAAGCAGTCCCTCCACTTCT
SEQ ID NO: 299	TGGAGGTATCCAGTATGAAATTTAGATAATACCTGCCTTC
SEQ ID NO: 300	GTTGAAATTAGAACTTAATGATATAATGCATCAATGAACT
SEQ ID NO: 301	ATAGTTCCTAGCACAAAGTAAGAATCCTTTCAATGTGTGT
SEQ ID NO: 302	GTGTATGTATTTATCTGTATTAATAGGAATCTTATGGGC
SEQ ID NO: 303	TCTCACTTAATCCTTATTAATAACTATGAAGCAGGTATTT
SEQ ID NO: 304	GAGTTTTCCAAGTGAGTTAAGTATAGCTTGAATACTTAA
SEQ ID NO: 305	ATATCCACAGGTTACATAGCTAGTATATAACTGAGAAATA
SEQ ID NO: 306	TATTTATATTATAAAACATTTCAACAATACAGATGTATAT
SEQ ID NO: 307	TAAAAAAGTAAAGGGCTCATGCAACCCCTACCTTCTCAAT
SEQ ID NO: 308	CTTCTTCACTTAGAAAAACAGCCTTAGCTGTCTGCTAT
SEQ ID NO: 309	CCTTTCAAAATATACTTCTGAGAAATGAGAGAGAGAAATG
SEQ ID NO: 310	GGGTAGAAGGAAGGAAGATAGGGTAAGAGACAGGAAGGA
SEQ ID NO: 311	TGGGAAAGAAATTAATATATCTTTTCTCTGTCTCTTGA
SEQ ID NO: 312	GCTCTTTCCATTACATGAATCAAAGGTAATGTTGCCATT
SEQ ID NO: 313	GACTCTTGAAATAAAGAAAGACCGATGTATGAAATAATTT
SEQ ID NO: 314	AGTCTATGGCATTTCAAAATGCAAGGTGATGTCTTACTA
SEQ ID NO: 315	GCCTTTGCTTTATTATTAGAAATGGGGAAGTGAGTATAGA
SEQ ID NO: 316	TTATCAGGAGATATATTAGGAAAAAGGAACTGGAGAAA
SEQ ID NO: 317	GAGGAGTATCCAGATGTCCTGTCCCTGTAAGGTGGGGGCA

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 318	CCTTCAATCAAAAGGGCTCCTTAACAACTTCCTTGCTTGG
SEQ ID NO: 319	CCACCATCTTGGACCATTAGTCCACAGGTATCTTCTTCC
SEQ ID NO: 320	AGTGGTCATAACAGCAGCTTCAGTACCTCTCTAAAGAGT
SEQ ID NO: 321	CCAGATATAGGTCAGGAAATATAATCCACTAATAAAAAAGA
SEQ ID NO: 322	CATTTTGACTGTAGTTGTTTGTGTTTTTGTGTCATTGTGACTA
SEQ ID NO: 323	TAACATTCTCACTCTTTCATCAGTAATCACTCAGGTTATT
SEQ ID NO: 324	GACCAACAGACTGTGGGAAAAATCAGAGAAGGAGGCATCC
SEQ ID NO: 325	GCTTACTAGCCTAAACTGAAATTGCTATAGCAGAGTGAAC
SEQ ID NO: 326	AGGTTTACAGATATTTCCACAAAGAGTAAAAGGATTGAA
SEQ ID NO: 327	TCTCCAGATCAATGCATAGGAAATAATAATGGACCATAAA
SEQ ID NO: 328	ATATTATGACGAACAACATTAGGATAAGTCCATATCAATT
SEQ ID NO: 329	ATCCAGTCATAAGCACAGACTACGTGAAGCACGTCCAAGT
SEQ ID NO: 330	GCAGGAGAAATGAGAGGAGCAAGAAAGAGGAGCCATTTGA
SEQ ID NO: 331	GAATAGCAGAAAAAGGAAAGCAAGTCATATTAACAAATG
SEQ ID NO: 332	TCATGCCAACAGTACAGATAACTCTGCTAATAAAGGTAGA
SEQ ID NO: 333	TAATACAGGTAGTAGCAGATATCTACATAGTAGTTAAAGG
SEQ ID NO: 334	GGCCATCAGTACAGAAGATTCATAAAGGAGAACCTAAAG
SEQ ID NO: 335	AGAATAATTTGTGAGAAGCTTAAAAGCTGAACTCTGAGGC
SEQ ID NO: 336	AACTACAATATCCTTTTGACTGTGGAAAGGGTGGTGAAAG
SEQ ID NO: 337	GTTCAAGGACATTTGAGCCAACATAGAGAGGAACATTTGCC
SEQ ID NO: 338	TGAGGGATATCTGTCTGTATGTTGTCCAGGATGGTGATGA
SEQ ID NO: 339	CATATAAATAACGTAGAGAAAACAGGAGGGGATAGAGATC
SEQ ID NO: 340	CAAAGAGGCATCAAGATAGGGATGTTTGTAAAGGATGAAA
SEQ ID NO: 341	CTGTTCTTCTCTGAGTAGCCAAGCTCAGCTTGGTTCAAGC
SEQ ID NO: 342	CATACTGTGGATCTGTAGCAAATTCCTGAAAACCCAG
SEQ ID NO: 343	TCTGACCCTCACATCAAGTTCTGAGGAAGGGCCACTGCC
SEQ ID NO: 344	GCCTTGAGATACCTGGTCCTTATTCTTGGACTTTGGCAA
SEQ ID NO: 345	ATAGGGCTTGTTTTAGGGAGAAACCTGTTCTCCAACTCT
SEQ ID NO: 346	CTGGTGCCATACTCTGAATGGGAAGAAATGATGGGATTAC
SEQ ID NO: 347	AGCAGGAGAGGATCAACCCATACTCTGAATCTAAGAGAA
SEQ ID NO: 348	TCAGATCCCTGGATGCAAGCCAGGTCTGGAACCATAGGCA
SEQ ID NO: 349	CTCCTCCCTACCACCTTAGCCATAAGGAAACATGGAATG
SEQ ID NO: 350	GACACAAACCTGGGCCTTTCAATGCTATAACCTTTCTTGA
SEQ ID NO: 351	CTACCTGACTTCTGAGTCAGGATTTATAAGCCTTGTTACT
SEQ ID NO: 352	TGAACCAACAAGCATCGAAGCAATAATGAGACTGCCCGCA
SEQ ID NO: 353	GAAAAGCAATAATCCATTTTTTCATGGTATCTCATATGATA
SEQ ID NO: 354	TAACACTTATCTCTCTGAACCTTGGGCTTTTAATATAGGA
SEQ ID NO: 355	TTTTCTGACTGTCTAATCTTTCTGATCTATCTGGATGGC

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 356	ATCTTCATCGAATTTGGGTGTTTCTTTCTAAAAGTCCTTT
SEQ ID NO: 357	GAAATTACAAATGCTAAAGCAAACCCAAACAGGCAGGAAT
SEQ ID NO: 358	ATTAGGCATCTTACAGTTTTTAGAATCCTGCATAGAACTT
SEQ ID NO: 359	TACAAATATTTGACTCTTCAGGTAAACATATGTCATAAAT
SEQ ID NO: 360	AACATTCAGTGAAGTGAAGGGCTACTTTACTTAACAAGA
SEQ ID NO: 361	TCTTTTCCTATCAGTGGTTTACAAGCCTTGTTTATATTTT
SEQ ID NO: 362	TATTTTGTCTGAGAATATAGATTTAGATACATAATGGA
SEQ ID NO: 363	CAAAATCTAACACAAAATCTAGTAGAATCATTGCTTACA
SEQ ID NO: 364	AGAATTTATGACTTGTGATATCCAAGTCATTCCTGGATAA
SEQ ID NO: 365	TTACTACTAGAAAATAGCCACAGGCTTCCTGCAAGGCAGCC
SEQ ID NO: 366	AGTTTGAACACTTGTATGGTCTATTCTCTCATTCTTTAC
SEQ ID NO: 367	ACTTCGTGAGAGATGAGGCAGAGGTACTACTACGAAAGCAA
SEQ ID NO: 368	TCTTGAGAATGAGCCTCAGCCCTGGCTCAAACCTCACCTGC
SEQ ID NO: 369	AATAGGATGTCTGTGCTCCAAGTTGCCAGAGAGAGAGATT
SEQ ID NO: 370	ATTAAGATCCCTCCTGCTTAATTAACATTACAAGTAAC
SEQ ID NO: 371	ACTTAAAGTAGCGATACCCTTTCACCTGTCCTAATCACA
SEQ ID NO: 372	TCTCAGGTGTTAACTTTATAGTGAGGACTTTCCTGCCATA
SEQ ID NO: 373	ATAGTTTCATATAAATGGGTTCCCTCATCATCTATGGGTAC
SEQ ID NO: 374	GGTATTTACATTTGCCATTCCTATGCCCTAAATATTTAA
SEQ ID NO: 375	TATTGATATTCTTGAAAATTCTAAGCATCTTACATCTTT
SEQ ID NO: 376	CTTTTATCTCCCTTCACCGAATCTCATCCTACATTGGC
SEQ ID NO: 377	TAGTGTCCTAAATTTTATAATTTAGGACTTCTATGATCTC
SEQ ID NO: 378	ATATGGTCACCTCTTTGTTCAAAGTCTTCTGATAGTTTCC
SEQ ID NO: 379	ACAATCTTCCTGCTTCTACCCTGCCCCACTACAATTTCT
SEQ ID NO: 380	AGTCACTGTCACCACCCTAAATTTATAGCTGTTGACTCA
SEQ ID NO: 381	CTGACCCCTTGCTTCACCTCCAATGCTACCCTCTGGTC
SEQ ID NO: 382	AGAAAATCCTGTGGTTTTTCGTGAAAGGATGTTTTCAGA
SEQ ID NO: 383	ACATATACTCACAGCCAGAAATTAGCATGCACTAGAGTGT
SEQ ID NO: 384	ACCCAAAGACTCACTTTGCCTAGCTTCAAATCCTTACTC
SEQ ID NO: 385	TGAGGTAGAGACTGTGATGAACAAACCTTGACAAAATT
SEQ ID NO: 386	TCCATATCCACCCACCCAGCTTTCCAATTTTAAAGCCAAT
SEQ ID NO: 387	AAGGTATGATGTGTAGACAAGCTCCAGAGATGGTTTCTCA
SEQ ID NO: 388	CTCTGGTCAGCATCCAAGAAATACTTGATGTCACCTTGGC
SEQ ID NO: 389	AACTGTGAACCTCCTTCAGCTAGAGGGGCTGGCTCAGAA
SEQ ID NO: 390	TGATGTTCTCTGACTTATCTACCATTTCCCTCCTTAAA
SEQ ID NO: 391	AAACAAAACCCATCAAATTCCTGACCGAACAGAATTCGT
SEQ ID NO: 392	CAGAGGTCACAGCCTAAACATCAAATTCCTTGAGGTGCGG
SEQ ID NO: 393	GAAGGCAGGTGTGGCTCTGCAGTGTGATTGGGTACTTGCA

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 394	CATGGAGGAAAACTCATCAGGGATGGAGGCACGCCTCTA
SEQ ID NO: 395	AGCTTGTTAAATTGAATTCATCCTTCTTATTCAATTCTA
SEQ ID NO: 396	CATAGTTGTCAGCACAAATGCCTAGGCTATAGGAAGTACTC
SEQ ID NO: 397	GCAGATATAGCTTGATGGCCCATGCTTGGTTTAACATCC
SEQ ID NO: 398	CTAAATAACTAGAATACTCTTTATTTTTTCGTATCATGAA
SEQ ID NO: 399	AGTGTTTAAAGGGTGATATCAGACTAAACTTGAAATATGT
SEQ ID NO: 400	GGATGGGTCTAGAAAGACTAGCATTGTTTTAGGTTGAGTG
SEQ ID NO: 401	TGCTGCCAACATTAACAGTCAAGAAATACCTCCGAATAAC
SEQ ID NO: 402	TATTGTGAGAGGTCTGAATAGTGTGTAATAAAGCTGAA
SEQ ID NO: 403	TTACAACATGATGGCTTGTGTCTAAATATCTCCTAGGGA
SEQ ID NO: 404	CTAAGTAGAAGGGTACTTTCACAGAACAGAGAGCAAAG
SEQ ID NO: 405	GTCTTGATTGCCAGTGACATGCACACTGGTCAAAGTA
SEQ ID NO: 406	CCCTATGTCTCCCTGATGGGCTAGAGTTCCTCTTCTCA
SEQ ID NO: 407	AAAGTTTCCCAAATTTTACCAATGCAAGCCATTTCTCCA
SEQ ID NO: 408	AACTGCAGATTCTCTGCATCTCCCTTTGCCGGTCTGACA
SEQ ID NO: 409	TAGTGCTGTGGTGTGTGATAGGTACACAAGAAATGAGAA
SEQ ID NO: 410	TAAGTAGCGTCAAGAAGTGAAGGCCCCTAAACTATGCTAGG
SEQ ID NO: 411	CATTGGCTCCGTCTTCATCCTGCAGTGACCTCAGTGCCTC
SEQ ID NO: 412	TGTTTATGTGTTATAGTGTTCATTTACTCTTCTGGTCTAA
SEQ ID NO: 413	CCTTTGACCCCTTGGTCAAGCTGCAACTTTGGTTAAAGGG
SEQ ID NO: 414	TTCTCTTGGGTTACAGAGATTGTATATGACAAATTATAA
SEQ ID NO: 415	TGGAAGTTGTGGTCCAAGCCACAGTTGCAGACCATACTTC
SEQ ID NO: 416	CTGCCCTGTGGCCCTTGCTTCTTACTTTTACTTCTTGTCG
SEQ ID NO: 417	AACTCAGATATTGTGGATGCGAGAAATAGAAGTAGATAT
SEQ ID NO: 418	TACAGAACCACCAAGTAGTAAGGCTAGGATGTAGACCCAG
SEQ ID NO: 419	TGAGCTCTCCTACTGTCTACATTACATGAGCTCTTATTAA
SEQ ID NO: 420	AAGCTAATAAGTAGACAATTAGTAATTAGAAGTCAAGTGG
SEQ ID NO: 421	AGCCCAATGTACTTGTAGTGTAGATCAACTTATTGAAAGC
SEQ ID NO: 422	CCAATACTCAGAAGTAGATTATTACCTCATTATTGATGA
SEQ ID NO: 423	GCTAGAATCAAATTTAAGTTTATCATATGAGGCCGGGCAC
SEQ ID NO: 424	TAATACTAATGATAAGTAACACCTCTTGAGTACTTAGTAT
SEQ ID NO: 425	ATGGTAATTCGTGAGATATGTATTATTGAACATACTATA
SEQ ID NO: 426	TGAAAGAGAAGTGGGAATTAATACTTACTGAAATCTTCT
SEQ ID NO: 427	GAGAGACACGAGGAAATAGTGTAGATTTAGGCTGGAGGTA
SEQ ID NO: 428	GTTGAGAGGGAAACAAGATGGTGAAGGGACTAGAAACCAC
SEQ ID NO: 429	CAAGTTCTGAACATGAGAAATTTTAGGAATCTGCACAG
SEQ ID NO: 430	TGCCATCTAAAAAATCTGACTTCACTGGAACATGGAAG
SEQ ID NO: 431	GGGATCCTCTTAAAGTGTTCCTGCTGGAATCTCCTCAC

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 432	GTTTCCTTCATGTGACAGGGAGCCTCCTGCCCCGAACTTC
SEQ ID NO: 433	TTGGATAAGAGTAGGGAAGAACCCTAGAGCCTACGCTGAGC
SEQ ID NO: 434	ATCTGGGGCTTTGTGAAGACTGGCTTAAAAATCAGAAGCCC
SEQ ID NO: 435	ACCGCAATGCTTCCTGCCCATTCAGGGCTCCAGCATGTAG
SEQ ID NO: 436	TATGGGGAAGCAGGGTATGAAAGAGCTCTGAATGAAATGG
SEQ ID NO: 437	GGTTGCATGAATCAGATTATCAACAGAAATGTTGAGACAA
SEQ ID NO: 438	AATGCAGGCCCTAGGCATGACTGAAGGCTCTCTCATAATTC
SEQ ID NO: 439	TAACGTTTTCTTGTCTGTACCCCATCATATGCACAACAA
SEQ ID NO: 440	TTAATTCCCAAACCTCATATAGCTCTGAGAAAAGTCTATGCT
SEQ ID NO: 441	CCCTATAGGGGATTTCTACCCCTGAGCAAAAGGCTGGTCTT
SEQ ID NO: 442	TCCTCACCATATAGAAAGCTTTTAACCCATCATTGAATAA
SEQ ID NO: 443	TAAGCTGTCTAGCAAAAGCAAGGGCTTGAAAAATCTGTGA
SEQ ID NO: 444	AGGATTAGAAGATTCTCTGTGTGTAAGAATTCATAAAC
SEQ ID NO: 445	ATTATCTTCTGGAATAGGGAATCAAGTTATATTATGTAAAC
SEQ ID NO: 446	CTCTCTGGTTGACTGTTAGAGTCTGGCACTTGTCACTAT
SEQ ID NO: 447	TCTTCAGTTAGATGGTTAACTTTGTGAAGTTGAAAACGT
SEQ ID NO: 448	CTACCCATGTGAGAAGGGTGGTGGTTTTGATGCTGC
SEQ ID NO: 449	ACTTTCCTAACCTGAGCCTAACATCCCTGACATCAGAAA
SEQ ID NO: 450	TACACTTTATTCGTCTGTCTCCTGCTCTGGGATGATAGTC
SEQ ID NO: 451	TACTCTTTGCATTCCTGTTTTTCTAAGTGACTAAAAA
SEQ ID NO: 452	AAAGGCCCTCCAGGCCAAGTTATCCATTCAGAAAGCATT
SEQ ID NO: 453	TATTGACATGTACTTCTTGGCAGTCTGTATGCTGGATGCT
SEQ ID NO: 454	TTTGGTCCTAATTATGTCTTTGCTCACTATCCAATAATA
SEQ ID NO: 455	GTTAAAAAACTACCTCTCAACTTGCTCAAGCATACACTC
SEQ ID NO: 456	TAATTAGTGCTTTGCATAATTAATCATATTTAATACTCTT
SEQ ID NO: 457	ACTAGTGTTCGTACTTTATGCCCATTCATCTTTAACTGT
SEQ ID NO: 458	GTATTTTTTGTTTAACTGCAATCATTCTTGCTGCAGGTGA
SEQ ID NO: 459	GCAGTGACTTATAAATGCTAACTACTCTAGAAATGTTTGC
SEQ ID NO: 460	TTATAAGCATGATTACAGGAGTTTTAACAGGCTCATAAGA
SEQ ID NO: 461	AGTATCCCTCAAGTAGTGTGAGGAATTAGTCATTTAATA
SEQ ID NO: 462	AGTCACCCATTTGGTATATTAAGATGTGTTGTCTACTGT
SEQ ID NO: 463	TGGTCATAAAACATGAATTCTAATCTCCCTCTCAACCCT
SEQ ID NO: 464	ACAGTTGAAAAGACCTAAGCTTGTGCCTGATTTAAGCCTT
SEQ ID NO: 465	CAACTACAGGGCCTTGAAGTGCACACTTTCAGTCCGGTCC
SEQ ID NO: 466	GTGGTTCCTTTGAAGAGACTTCCACCTGGGAACAGTTAAAC
SEQ ID NO: 467	TGGAGGAAATATTTATCCCCAGGTAGTTCCCTTTTTGCAC
SEQ ID NO: 468	GCCTGGTGCTTTTGGTAGGGGAGCTTGCACTTTCCCCCTT
SEQ ID NO: 469	TCTCATTCTTTGAGAACTTCAGGGAAAATAGACAAGGAC

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 470	CAAACCTTTCAAGCCTTCTCTAATCTTAAAGGTAACAAG
SEQ ID NO: 471	TCAACAAAGGAGAAAAGTTTGTGGCCTCCAAAGGCACAG
SEQ ID NO: 472	GATGCAACAGACCTTGAAGCATACAGGAGAGCTGAACTT
SEQ ID NO: 473	CATCTGAGATCCCAGCTTCTAAGACCTTCAATTCTCACTC
SEQ ID NO: 474	TATCTTAACAGTGAGTGAACAGGAAATCTCCTCTTTTCCC
SEQ ID NO: 475	AACTCATGCTTTGTAGATGACTAGATCAAAAAATTTCAGC
SEQ ID NO: 476	TCAAAGGAAGTCAAAGATGTGAAAAACAATTTCTGACCC
SEQ ID NO: 477	TGCCTTCACTTAAGTAATCAATTCCTAGGTTATATTCTGA
SEQ ID NO: 478	CCCTACCTTGTTCAAAATGTTCCCTGTCCAGACCAAAGTAC
SEQ ID NO: 479	GCACTTACAAATTATACTACGCTCTATACTTTTTGTTTAA
SEQ ID NO: 480	CTTTAGTTTCATTTCAAACAATCCATACACACACAGCCCT
SEQ ID NO: 481	TAGGGACCACAGGGTTAAGGGGGCAGTAGAATTATACTCC
SEQ ID NO: 482	CTCACAATTAAGCTAAGCAGCTAAGAGTCTTGCAGGGTAG
SEQ ID NO: 483	GTTGAAAGACAGAGAGGATGGGGTCTATGCCCAATCA
SEQ ID NO: 484	GCTTGTCTAATTTTATATATCACCCACTGAACATGACCC
SEQ ID NO: 485	AATATTGTACACGTACACCAAAGCATCATGTTGTACCCCA
SEQ ID NO: 486	TGTGAAGTGGTGGATTTGTTAATTAGCCTTATTTAACCAT
SEQ ID NO: 487	TGACACATATGACATTTTAACTATGTTCCAGATTTTGA
SEQ ID NO: 488	GCAAGGAATCATTCAATGTTTTCTAAATCTATTACTGCAT
SEQ ID NO: 489	CATTTTCATAGGTTTTCTCGATTGATCATTATTCATGAT
SEQ ID NO: 490	AAAGTGATCAAGATATTTTAGTTTCAGGCTCCAAAATTT
SEQ ID NO: 491	CTTTACAGGCCGAGAAAAATGAATCTGAATTCCTGACCTC
SEQ ID NO: 492	TCCACTCAAGCCTACATTCTGCTATAATGCAATTTCAAG
SEQ ID NO: 493	AACTGCTTAAAATTAATGGCACAAGTCATGTTTTTGATGT
SEQ ID NO: 494	CTGACTGTGACGTAGCAATAAAGAAACCCACGTTTCATAT
SEQ ID NO: 495	CTGGCCCACTGCTTGGAGGAGAGCACTCAGGACCATGAAC
SEQ ID NO: 496	TTCTGAAATGATAAAGTCAATCACAGGAAGGCACCTGGAC
SEQ ID NO: 497	ATCATTCTCTTTCCCTTCCTCTATGTGGCAGAAAGTAAAA
SEQ ID NO: 498	GGAGATAATAATGTGTTACTCCCTAAGGCAGAGTGCCCTT
SEQ ID NO: 499	CAATTAAGTGGCCATGTGACTGGTTGTGACTAAAATAAT
SEQ ID NO: 500	CACTAAATCAATATACTTCTCAACAATTTCCAACAGCCCT
SEQ ID NO: 501	CTAGGCTCCTGAGTTTGCTGGGGATGCGAAGAACCCTTAT
SEQ ID NO: 502	CCGAGGACCCCGCACTCGGAGCCGCCAGCCGCCCCACCG
SEQ ID NO: 503	TTGGAAGCACAGGGTGTGGGATAATGCTAATTACTAGTGA
SEQ ID NO: 504	GTTCAAGTATGCCTTTGATTTTACAATAATATTCCTGTTAT
SEQ ID NO: 505	AGATTCCATGAAGTATTACAGCATTGGTAGTCTTTTTCG
SEQ ID NO: 506	TATTTGCTCTGAAATAAGACATAATTTGGGGTGAGAAAGC
SEQ ID NO: 507	ACTCATGATATTTGGCTCTAGAATACATGCTCTGAATCAT

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 508	TCCAAGATGAAGTGGCTACTAACTGACAGAGGGCATAATT
SEQ ID NO: 509	TATTCACAGTAACTCTGTGCCTCAAGTACTATTGTAATAC
SEQ ID NO: 510	ACATCCTCAATCTACACACTAGGATAGTATAAAAAGTAATA
SEQ ID NO: 511	GTCTACCCATATGTGACCTTCATGTCTTTGCTCTAAGCCC
SEQ ID NO: 512	CGTGTAAATCCTTGACAAATGCATCTCATCTATTTATTTCCC
SEQ ID NO: 513	TCTGAAAGAGACTAACCTTCCCTCGCTTTGCAGAGAAAAGA
SEQ ID NO: 514	ATGCATGGATTCTCTTGAAAAATGTTTCTGCCATGATGT
SEQ ID NO: 515	TAGTTGAAGCCTACTGTGTTTCAGGGCCGTGAGCCAGGGC
SEQ ID NO: 516	CAACGTGGAGAGCTGTCTGGCACCATTCTTCTCTGCTGT
SEQ ID NO: 517	ATCCTCAAAGGAGCCTGGCTTGGGCTAACCAAGGAAGAACT
SEQ ID NO: 518	TGCCTGGGACCTGCCCAAGCAAAGTAATAATCTGAATG
SEQ ID NO: 519	CTGGTGTGTCCAGTGTGATCCCTGCACCCATGCCCGGAGC
SEQ ID NO: 520	CTGCCCCCTGCAGCAGGAAGGGGCTCTGGAAGGGTCTGA
SEQ ID NO: 521	TAGCTGCTGCCCCACTATGCACCATCGCTTATCTGTCTTT
SEQ ID NO: 522	GAAACCCGAAAAATGTCTCGTCTCTTCTTAAGTCTGGG
SEQ ID NO: 523	GCTGAGAACATGACTCTGCTTGGCGTTCCATTTAATTGAC
SEQ ID NO: 524	GAGAGGGTGTGCATTTGAAGTATAGATTTGTTAAACATAG
SEQ ID NO: 525	CATCAGGCAAAAATACTTCGATGGGACTGTGTTCTTTTCAG
SEQ ID NO: 526	TCTAAAGTGATGTAATGTGCCACGGAAATCTAATCCCT
SEQ ID NO: 527	CGTGCAGAACAGCTCTGTCTTCCAGACACTGTGCTTT
SEQ ID NO: 528	ACCCCTGAGCACCTCAGTGTCCGTGACTGTGGAGCGGAGG
SEQ ID NO: 529	CTGCCTGGGACACGTACGGCTGCCAGTGATCCTGAGCGC
SEQ ID NO: 530	CACAGCCGGATGGTGTGGGAGCTGGCACTGCCGGGGCTCC
SEQ ID NO: 531	CGTCTTGGCAGAGGCTCCCTGTTCATCAAGGACCTGAGGTT
SEQ ID NO: 532	GACCCACAAAGATGAGCGGTCCCCTTCCCAATTTTCGG
SEQ ID NO: 533	TCAGGAAGCCGGTGTCTCAGCAAATTTATCTGAAGCTCTTG
SEQ ID NO: 534	GAGGCTGCAGAGGAACATCGTTTGGTCAAATGTGAAATGT
SEQ ID NO: 535	CTAGCTTCTAGAAAGTGTGCAATTTGGGGACCAAGGGA
SEQ ID NO: 536	GGAAACACTTCTTTTCCCTTGACAAAGGACATCCTCTGC
SEQ ID NO: 537	GCATGTGCATAAACACTCGTGTGTGTCTTTTATCCCA
SEQ ID NO: 538	CCAAATCTCTATACATGTCCATAGAGAGAGGCAGACGTAT
SEQ ID NO: 539	GGGTGAAGACAAGGGCTCAGAGCTTGTCTTTTATACAC
SEQ ID NO: 540	AGATTCATCTTCATGGCAGGACTTCAGGCAAGAGAGGCC
SEQ ID NO: 541	CTCACCCCTTAGCAGGACCTGACGGAACTGGGTACAGGC
SEQ ID NO: 542	GGTTGGGAGACAATGGGTGGCCCTCGGTGTGGTGTCTCTC
SEQ ID NO: 543	AGAGTCTAGAGGGCCCGTGGGACGGGAGTCTGGGAACC
SEQ ID NO: 544	GCGGCATGTCCGGCTTACCCTGCCAGAAATCACAGCCTC
SEQ ID NO: 545	ATGGTTAAAAAATCTCCTACTTAAGACTCCCAGACCCCT

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 546	GGGTTGAAGACAAGGGGCTCAGAGCTTGCTTTTTATACAC
SEQ ID NO: 547	AGATTCATCTTCATGGCAGGACTTCAGGCAAGAGAGGCC
SEQ ID NO: 548	CTCACCCCTTAGCAGGACCTGACGGAACTGGGTACAGGC
SEQ ID NO: 549	GGTTGGGAGACAATGGGTGGCCCTCGGTGTGGTGTCTC
SEQ ID NO: 550	AGAGTCTAGAGGGCCCGTGGGACGGGAGTCTGGGAACC
SEQ ID NO: 551	GCGGCATGTCCGGCTTACCCTGCCAGAATCACAGCCTC
SEQ ID NO: 552	TGAGATTCCAGGGCTGGTTCCACAACGGCCGGCATCGGCC
SEQ ID NO: 553	CTGAGTCACTAACAAAGCTCAGGCCTGACCACAGGACATT
SEQ ID NO: 554	GGCTGGCCTACCTGCCACGGGGCCAGGGCTGGGTGCTTTC
SEQ ID NO: 555	GGGCTCTGGACGCTGGAGGCCTGAGGCTGCACCCAGGTT
SEQ ID NO: 556	ACAGTGGCCACTCACCCACTGGGCCACATCCCCACAGGC
SEQ ID NO: 557	ACTCTGCCAGCCTTGTATGCCTCGCTGAGACAGAGGTCT
SEQ ID NO: 558	AGCCGGGCTCTGGCCCATCCAGGGCTCCCCAGCAGC
SEQ ID NO: 559	CCTTGGAAAGTCAGTCAGCAGGTCAGGACACAGTTCAGCCC
SEQ ID NO: 560	TTACATGCAGTTGGTCTTCTCCTGTGAATGGGAAACTGA
SEQ ID NO: 561	CTGCATCACAGAACAGCTGCATTTCTAATGTGAGGCTTCT
SEQ ID NO: 562	CAGCCTGGGAGGCTTGTCAACCTCCTTTGACAAGCACGCC
SEQ ID NO: 563	AGAAACTGGGCTCCAGGGCATGGAGGCTGCCTGTGGCCA
SEQ ID NO: 564	TCCCGGCCTGGAGGAAGTCTTATTAGCCTCATTTATGGA
SEQ ID NO: 565	TCCTGCCAGCCCCCTCACGCTCACGAATTCAGTCCAGGG
SEQ ID NO: 566	AATTCTAAAGGTGAAGGACGTCTACACCCCAACAAAAC
SEQ ID NO: 567	GGAAATATTAGTCCCTCTGCCTGGGACAAGACCACCGAA
SEQ ID NO: 568	AAACACACCTCTGAATGGAAAGCTGAGAAACAGTGATCTC
SEQ ID NO: 569	ACTGCACCCCTCCCTTCCCGTGCCTGGCAATTTAACGGG
SEQ ID NO: 570	TGCCTTCTACCTTGACCAGTCGGTCTTGCGGGGTCCC
SEQ ID NO: 571	ATTTCTTCATCTTGTCTTCTAGCCTGGAGACTTCTCGG
SEQ ID NO: 572	AATGCCCGAAAATTCCAGCAGCAGCCCAAGATGGTGGCCA
SEQ ID NO: 573	CGTTGCAAAATGCCAAGGGGTAAACCTAAAAGTTAAAGG
SEQ ID NO: 574	ACACAACCCCTGTGCAAGTTTCATTCGGCGCACAGGGGC
SEQ ID NO: 575	TGCAAGAACTAATTTAGCATGCAAGGACGGGGAGGACCGG
SEQ ID NO: 576	GCCACGAGGGCACCCACGGGCGGACAGACGGCCAAAGAAT
SEQ ID NO: 577	ACCCCATATCCAAGCCGGCAGAATGGGCGCATTTC AAGA
SEQ ID NO: 578	GCCTGGGGAGACCACGAGAAGGGGTGACTGGGGCGCGCG
SEQ ID NO: 579	CTGCAGTAGGGGACAACCTAGGAAGCCGGCAGGCCACACG
SEQ ID NO: 580	GAGTGGGTCCCCGGGATTTAGGGGTGAGGTGGAGGTGG
SEQ ID NO: 581	TCCCCGCCAGGGAAGAGGGGTGCAGGGGGCCCGTCCGCC
SEQ ID NO: 582	TGAGGGCGCGCCTGCCCTGCGGCGGAGTTGCCCTGTA
SEQ ID NO: 583	AAACGCCGGGAGCAGCGAGGGGCAGAGCCCAAGCCATC

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 584	TTGTTAAGCAAAGATCAAAGCCCGGAGAGAAATGGGAGCG
SEQ ID NO: 585	CAACTTCAACAAAACCTCCCTGTAGTCCCGTGTGACGTTAC
SEQ ID NO: 586	CTGCTACTGCGCCGACAGCCCTCTGGAGGCTCCAGACTT
SEQ ID NO: 587	GCTCTTCTGCCCTCGCCGGAGCGTGCAGGACTCTGCTGCT
SEQ ID NO: 588	TCCGCGCTCGGCTCTCGCTTCTGCTGCCCGCGCTCCCTC
SEQ ID NO: 589	TTTCCACTTCGCAGCACAGGAGCTGGTGTTCATGGCTGG
SEQ ID NO: 590	GGTCGTTGAGGAGGTTGGCATCGGGGTACGCGCGGCGGAT
SEQ ID NO: 591	TGTCCTACTTCAAATGTGTGCAGAAGGAGGTCCTGCCGTC
SEQ ID NO: 592	TCGGGCGGCTCTCTAAGACTTCCCTGCAACTTGTGCCC
SEQ ID NO: 593	ACCCACGTTTCTTTGCTACTCACCCCTCCCTTCTCTCC
SEQ ID NO: 594	CTAGAACTTTGAAGTTTGCCGTGGTGTCTTAGGGATCCG
SEQ ID NO: 595	AGAAGGGGGTCCGGGAGGGGTGCCTTCGGGAGAAGCCAGT
SEQ ID NO: 596	CAGGGGCACCCCAATGGGCCCGAGGGTCCGGGCTGGCAGG
SEQ ID NO: 597	GGGTGCGCTTTGTGTCCCCCGCTGCGCCCCAGCCGGCT
SEQ ID NO: 598	GCCTCAGCGGCCGGGAGCCGCCAACTCCGGGGGAGGGGG
SEQ ID NO: 599	AAAGTGCAGTAATACCCCTTGATCAGAGTTGATGACTTGAA
SEQ ID NO: 600	GAGAGAAATAAAGTAGTTGCTCTATTTGTAATTGAAAAG
SEQ ID NO: 601	GGTAGCAGTGATTGCTGTATATTTGTGAAAAGGAGGCAAG
SEQ ID NO: 602	TGCTGATAATGGAAGTGCAGTGGGTTAGCTTTGTTCCAT
SEQ ID NO: 603	CCGTTCTACCGTGACTAGTATGGAATTGTGGGAACCAGAA
SEQ ID NO: 604	TTAACATCAGTGTCAACTGCAGTGTGTTTCTGAGTAATA
SEQ ID NO: 605	CATAACTCCATGCTCTCAAACCAATCACTCCTTCATTTCAT
SEQ ID NO: 606	TTCTCCTATGCTGCACCAGAAAGGTTTTGTGGGTTATCA
SEQ ID NO: 607	ATCGTTTACGATCTTTAGGAAATATCCAGAGACTGCATTG
SEQ ID NO: 608	TTTATTAAGAGCAAAAAAGCCTGTTTCGTTAGCCAGTCA
SEQ ID NO: 609	TGTTTCATATGCCTAACTTAATAAATTCCTCATAACAGAAA
SEQ ID NO: 610	ATAACTTTTAAACCCAAACACCTAGAGATTCATTATGTA
SEQ ID NO: 611	TTCTTACCATTAAGTCTTCCAAATGATAATTTATTATAAAA
SEQ ID NO: 612	TATGTAAGGACAACCTCATTATATGCTTGAAGAAATGTT
SEQ ID NO: 613	AATCTTAAAAGTGACACTAGTCACATTCACACGGTTAAA
SEQ ID NO: 614	ATTTTGAAAACCTATTCCTTTATCTGGAATGAATGTAAACC
SEQ ID NO: 615	TTGCATTAAGGGCACCAGAACTTATAGAAAACCAAAAAG
SEQ ID NO: 616	TAAAAGACAGTGAAGTGAACAGTAATTAACATTACATCCA
SEQ ID NO: 617	CAAAAACTGTGTTTATCATATACCAACATTTTCAAGTT
SEQ ID NO: 618	TCTCAGGATATTTGTTCTCTGACACAAATACACCAGTCA
SEQ ID NO: 619	TAGCTTTACATCTCAGAATGAATCAATGTGGGGCAGAAA
SEQ ID NO: 620	AGACCTATATACCTATAGTGCCTAATAGACAATAAGCCAC
SEQ ID NO: 621	TCTCTCCCTGCCTAGACTAAGGTAAGTGGGTCTTACCTT

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 622	CATCCTGCTTTTAAAACCCTTAGTGCTCAGCGGCTTGCTCT
SEQ ID NO: 623	AGCTTATAAACTTCAGAGTAATGTAGCACAAATGCTGTGC
SEQ ID NO: 624	AACTTGAATAAACTTTAAACGTTGATTGATTCTTTCCC
SEQ ID NO: 625	GACAGGCTTAGAGTCCATAACAAACAATCTTAGCTGGAAA
SEQ ID NO: 626	TGCTCAACAACACTTGTGGAAGAGCAGGGCAAGCTATTTTC
SEQ ID NO: 627	TTACAACATCACTGTAGACATTACTTTTACCCACAGTGCC
SEQ ID NO: 628	ATCCTAGTTGTATATACTTCTTGGATAAAGTATCTTCGTA
SEQ ID NO: 629	ATTTTGGGGAGTGCCATTCCTGCAGGTCTTGAAGACAGG
SEQ ID NO: 630	CACACAGCCAATGAACTGACAGAGCCAATGCAACCAAAA
SEQ ID NO: 631	ACGACTTCAATCAAGAGAAACAGGCAGGTGAGAGTGTGAA
SEQ ID NO: 632	CTGGTTATCAGGGTTCATAGCACATAGGTTTGACAACCAC
SEQ ID NO: 633	TTTATTATTCAGCTGGGTAAGCCAAGTGACAGTCTTCCCC
SEQ ID NO: 634	GTTTTATTCTAGGAATCAACTGCTTTCTAAAAATGTCTAA
SEQ ID NO: 635	TTTACTGATGGTACTTATTCCCCCAATTATTGATTATTGA
SEQ ID NO: 636	GCATTTAGGAATATTC AATATTGATACTAAGGTCATCTTT
SEQ ID NO: 637	TACTCTGTAATGTAGTAATCTTTATGAAGAAATAAATTTG
SEQ ID NO: 638	ATTTTGAAAAATGTTTCACTGCATTTTACTATAACAAGCT
SEQ ID NO: 639	ACCACACATTCATCAAAAAATACCTCAAAGAAAATTCCTGC
SEQ ID NO: 640	GTTGTCACAATAAACTCAGTACTGAGTAAAAATATCACAAA
SEQ ID NO: 641	GAGTATATATTGTATTACTTACCTGATGCGCAAGACCCA
SEQ ID NO: 642	AAAATGACAGCAACATAGGTGCCACCTGAGGTCCACATCT
SEQ ID NO: 643	TGGAGAGAGTGGGGTTAATCTGTTACTACACTTTGCTACT
SEQ ID NO: 644	ATTTCCATCATTTTGTCTTTTCAGTAAGCATGTACGAAGTA
SEQ ID NO: 645	GAGATGAAGATGGTACATCAGTAGGGAGCCCTCTACTGG
SEQ ID NO: 646	TCTAATTCATCAAAGTATTCGGGTTGATTCCAGGTACGT
SEQ ID NO: 647	ACAAACTCGTTTTGTACAGAGAGGAAAATATTAACACC
SEQ ID NO: 648	ATGTTAATTATAAACACTGTTATAAGTTTTACAAATGTAA
SEQ ID NO: 649	TCCACTGGCAGAGAGAATATATGTTTCCATTACGGTCCCA
SEQ ID NO: 650	TCAAAGGTTTTCTATCACGTTTTCTATTATTTACTCACAT
SEQ ID NO: 651	AAAAACAAGAGTCACACAACCTATGCTCCACAATATCTGC
SEQ ID NO: 652	ATAGGTTATTCTACAATCGACACCAACTATCAGCGGCTTT
SEQ ID NO: 653	ATTGAATTAATGATGGCTTGATTATCCAGGAATCAGCCA
SEQ ID NO: 654	CTTACCATAACAGAGTAATCTCTAGCTTATTTCCAAGGATA
SEQ ID NO: 655	ACCTAAAATTTAACTAGAATCACTTTTCAATGAAGCTGCT
SEQ ID NO: 656	TAACTAAGAGCCTTTGATCTTGCTTATTTCTGATAAAAT
SEQ ID NO: 657	AAATAATAATTCACAAGGAAATCCTTATTGTTTATTTAAA
SEQ ID NO: 658	GTAATATGTAGGTTAAACAGAAATGTTGGTTGAATCATGT
SEQ ID NO: 659	TGCAGACACTAATCAAACCAACAGGGCCAATTAATAATG

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 660	TAAAGTGCAATGGGACAGAGCAACTTCATTTTCACAAACA
SEQ ID NO: 661	TAATCTAATTGCCAGAAATGCTTGCCCATGCAATGGGAG
SEQ ID NO: 662	AGTTGACAATGACTGCTTAGTTTAGGGTTTGAAGTAAAC
SEQ ID NO: 663	CAGATGGCAGGTATTCTGTGAATTAACACTGATGCTTCTG
SEQ ID NO: 664	AGTCAAGTTCAGAAATGATCTGTTATGACCCCATGAAACG
SEQ ID NO: 665	GGGATGCTCTGATACATCATTGATGATAAATGATAGAAAA
SEQ ID NO: 666	TAGCTGTATTGCTTGATAGCTTCATAGCTTGATAACCATT
SEQ ID NO: 667	TTTAGCAGGAATTAACACAGGTATATAAATGAAGAAAA
SEQ ID NO: 668	TTGATTGTTTATGAAGCTGAGATTGTTTACTGGTTTCGAG
SEQ ID NO: 669	TCTGTGTTTTATGTTTGGGAACATGAGGGAATCAGTTCT
SEQ ID NO: 670	TTCTTAAGCTTTCATTTTCCAGTGGTGAATGTAGAGAGA
SEQ ID NO: 671	ACGGTAACTGAATAAACTTAAGAAGTAAAGTTTTC
SEQ ID NO: 672	TCAATATGTAATAATGATCAATTCAGACACCTTTATATGG
SEQ ID NO: 673	TGCTCTTTTCATGCTGTAAATAGAGCATTGCATGAAAGAT
SEQ ID NO: 674	TTCATAGCACAGTTTATAAACCTAAGAAAGCAAAGATGAA
SEQ ID NO: 675	AACCAAGCAGGATTCATGACTAAAAAGTGATTTGTAT
SEQ ID NO: 676	AGATAGAGAATTTCAAGAAACCATCTTTATCAGTGCAC
SEQ ID NO: 677	CCAAGAATGAAAAGATGCACTAATTCGACTGAAAGCCAAG
SEQ ID NO: 678	TCATAGTTGAGACATATAACAACCATAAAGGTCCGCATAT
SEQ ID NO: 679	AGGAAAGGGTGGAAAGGCAAGCAGCGGGAGTGTGGCTG
SEQ ID NO: 680	CTATAAATTGACCTATCCTGTAAAAAAGGATGTCACAGCA
SEQ ID NO: 681	ACAATTGACCTAAGACTGTAAATTGAAATTGACTATAAAA
SEQ ID NO: 682	GCAAGACTGGGTATACTATTAATAGGAAAAATGAACTTC
SEQ ID NO: 683	ATTGCTTTGATATTGATTGAATCAGAGAAAAATCCTAAG
SEQ ID NO: 684	TAGATTATGCTGGCAAATCTCAGTATCAGAGAATTATAT
SEQ ID NO: 685	ATTCAGAAATGGAATAGGAAGATATTTATGTGCCATCCTG
SEQ ID NO: 686	GTTTGAATTATTATTCAAACAGTGTATGTTGTTTGTACT
SEQ ID NO: 687	AATGCAACAGAGACAGGTATTTATAGCATCTGTTTCCAT
SEQ ID NO: 688	TTAATATCCAAATATGTATGGACACATACAATTGTACAT
SEQ ID NO: 689	ACGTCTACCGTCATTTTCGTAATTATTCGGTTTCCCTGTC
SEQ ID NO: 690	GGAGCGCTCCTGCGCGCCTTGTTCGTTAGGATTTATTTTT
SEQ ID NO: 691	GGTGGCTCCCTAATGCCTGCTCGTTTCAGGTCTCAGCTCT
SEQ ID NO: 692	CCTTAGTGTGTTGAGGACGCTGCAGAAGGTACAGAGGAGA
SEQ ID NO: 693	GACCAGATGGTAGGACAGTCAATCTCCTCTGCGTCTCCGC
SEQ ID NO: 694	CGTGAGGCATGGAGTTTTTGTCTGCCCTGCCTGGTTAG
SEQ ID NO: 695	TTTAAGTCTCTGGCACCGTGCATAGCAGAATTGGTTGGGA
SEQ ID NO: 696	TCTTTCTCCAAGTGCCCTATGTTGGCACATCTCTGAAAT
SEQ ID NO: 697	TGCGTCCCGCCAGGTAAGCAGCTTCCCTCTCAGTGCCT

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 698	GGGTGTATGTAGCTGGCAGAAGTGGGACTTGGTCGCAACC
SEQ ID NO: 699	CGTGGCGAGTGGGCGGTAGCTGCTCGTAGAGCGTGTGAAA
SEQ ID NO: 700	GTTGGCCCTAAAAGTTATCATTTCATGCTAGTTTGACCAAT
SEQ ID NO: 701	AAGTGGGAGGAGCTGGGCAAGAAAGTCCACCCCTTTTCT
SEQ ID NO: 702	GCCGAGCCGAAGTCATCTGCCAATCAAACAGCCACAGGG
SEQ ID NO: 703	CGCGTACCTAATGGGAGACAGACAGGTGCCTTTAAAGCGG
SEQ ID NO: 704	TGGGGAAGCGGAGGAAGGCATGGAGTGTGGGCGTTAGGG
SEQ ID NO: 705	GCATATTCTGCCTTGAAGTCATTGGTTGGTCTGGAAGTG
SEQ ID NO: 706	AATTGGTCTGGGGAGGAGCTACGACAGTCCAGGGGCGGG
SEQ ID NO: 707	GTGTCGTGCTGATTGGATGTATCCGCCCCCTCTCTAAA
SEQ ID NO: 708	CAACACGCCAGCGCGAGGACCCGAACGTCAATCAAGAGAC
SEQ ID NO: 709	GCGTTCGATTGGCCTCCCGCGCAGGCTGCTAGGATTGGCT
SEQ ID NO: 710	CCCTGCCCCCTTTCGCGGATTGGGTGATCGCTCCAAGGCG
SEQ ID NO: 711	CTGACCCTTGGAGGCTTCTATTGGTTCTGGCAGGGATG
SEQ ID NO: 712	TCCCGAATATAGGCCAGTCATTGCTCCTGCTGAACGTCGC
SEQ ID NO: 713	CCCCTCCTCTTCTCTGCTCTGGGCGCCGACCCGCCCCCG
SEQ ID NO: 714	GCTCAAGGGAGGCCGCGGCTGCGGATGGTCCGCGGA
SEQ ID NO: 715	TGGGGAGTGGGCCCGGGTTGTTCTGACGACGGGGTTCG
SEQ ID NO: 716	CCCGGGCGCTATCGCGATAGCGGCGGAAGCGGAAGTGGG
SEQ ID NO: 717	CGGGGAGGCCGAGCGCCCGCCCTTTTCTCGCGCCCG
SEQ ID NO: 718	CACAGGAGCTGGCGCCGCGCTGAGGAGCGTATCGCGACA
SEQ ID NO: 719	GTTGCCGACTCGCGCTCTCGGCTTCTGCTCCGGGGCTTCT
SEQ ID NO: 720	ACTCGGAGCTCGGATCCAGTGTGGACCTGGACTCGAATC
SEQ ID NO: 721	GGCTCCTCCTGTTCCGAGCCGAAGGCCCGCCCTTAC
SEQ ID NO: 722	CTTCCGGAGCCCGTCTGTTCCCTTCGGGTCCAAAGCTT
SEQ ID NO: 723	GACCCCGCTCATTCTCACGGCGAGCTCCAGACCCCGCC
SEQ ID NO: 724	AGAACTCAAGCTCCCGATTGTGCCCGAAGGAACCCGAAG
SEQ ID NO: 725	ACTATTGCCGAAGTGAGCCGAAGTTTGTGGCCCCGCTTCC
SEQ ID NO: 726	ACATGTGGCTCCGCCACACTGGCCTCAGCTCTCGTTCT
SEQ ID NO: 727	ACAGTGACCCTAAGGACTCGACTACCTCCGAAGAAAGCCG
SEQ ID NO: 728	CTTGTACCAACTATCTACGAAGTAAACCGAAGCTTGTGG
SEQ ID NO: 729	TATCTGGCGAACCTGTTGACTCCGCCTATCATCCTAGCGT
SEQ ID NO: 730	GGCAAGTCGCTTTCGCCCGCCCTTGTAAATACTCATG
SEQ ID NO: 731	CTCCTCTACTTGGGAACCTGAGGATCGTCACCCTGGCCCG
SEQ ID NO: 732	TGGCTCCGCCCACTGAGCGCACCTCCCTCTGCCGCTTC
SEQ ID NO: 733	TCCTTGCTCCACCCCTCATGCCGACCCCTCGTCAACTT
SEQ ID NO: 734	TCCACCGATAGAACCAGCGAGTCACCTCATAAACAGTAAT
SEQ ID NO: 735	CGCTCAGTCCGCCTCCTTGCCTCCCTTCAAGATGTCCAC

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 736	GCCGTCCACTCTCCGCTCGGGCGGGCTCACCCCAATTGGG
SEQ ID NO: 737	CGACCGAACCCACAGCCGAAAGCCCCGCCCTGGACAC
SEQ ID NO: 738	CTCCGAGCGCCAGCGCACCCAGTTGGGGAGTTCCCGCCC
SEQ ID NO: 739	AGCCCCGCCTCTCCCGACGCAATAGGTTCCGGCGTTCGG
SEQ ID NO: 740	AGCAATTTGACGTTCCGGTGTCTCCGGCTCGGCCGAATCC
SEQ ID NO: 741	TGCCCCCTCCCGAGCACAGGAAGTTCGGCGTTCGGGCGTC
SEQ ID NO: 742	TTTCGGACCTCCTCGCTCTCAGACTCCACAGTACAAAAC
SEQ ID NO: 743	CGAGCCTTCGCTCCTCCTTTCCGAACTGTGATTTCG
SEQ ID NO: 744	GAGGCTAAGGCACCGCCGAGGCCACACCTCTCCGGACG
SEQ ID NO: 745	GCGTCCCCCTTCGGGTGTCCCGTCAGCGGTGAGAAGCTC
SEQ ID NO: 746	CCTTACAAAGGTCCATTTTGGCACACCTCTTGCAAAGT
SEQ ID NO: 747	GGAGCGTGAAAAACAACTCCGCAAGCGCGGCACACGC
SEQ ID NO: 748	ACCCGCTCTGTGCCCGCACTGCCGTACCTACCATTGCGCC
SEQ ID NO: 749	GGTCCTCAGCATCTGCATATGTAGCCCCCTCCCGCTGGTCA
SEQ ID NO: 750	CCCAACCCCTACCCCAATCCATCTTAGAGCTGATTCTCT
SEQ ID NO: 751	ACTCCAGTGATTCTTCTTATGCTAGGGACTCGAGGACCC
SEQ ID NO: 752	GAGAATTGAGAAGTCAGTGTGGAGGGGATGTCCAGTAC
SEQ ID NO: 753	TTTCTGGTTCGCGTTGGCTGCATTGTGGAGCTGAGGGATG
SEQ ID NO: 754	TAGCTTCTTAATCTCCTTCTTTAGGTCAGCCTCATACTTT
SEQ ID NO: 755	TTCTCCCTGGGACCCAGCAGTCCACTCTCCAGTTCCTC
SEQ ID NO: 756	AAAGTCAGACCTCAGGACCCAGGAACGGGGCCACAGCT
SEQ ID NO: 757	TCTTGATTGGTCCCTCAGCCGCTGCAGATGGGAAAAGCA
SEQ ID NO: 758	TAAGCTGCCTCTTGTCCTTGATCTCGTTGGACGCTACCCA
SEQ ID NO: 759	GGCTCTGGGCTCCTACCGTCTCAATGAGCTTCCGGTTGTC
SEQ ID NO: 760	TGAGGACCTCTGGGGTCTGGCCGCTCTGCCTCCGCCCTT
SEQ ID NO: 761	CTGCCTCTTCACTTCCCTTAGGTGCAGAACTTACTTCT
SEQ ID NO: 762	CGACCTGAGCCTCGTGACCTACTTTCTGAGCTCTGAGTC
SEQ ID NO: 763	TCAAAGGTGGGAAAGGAGCTGACTAAGGGCCAGCAGACAC
SEQ ID NO: 764	CCGTTCATTTGCTGTAGAGAGTGCAGTTGGCAGGGGGC
SEQ ID NO: 765	GCTGTAAGCTTTGGTTTTGGTCTCTCGTTCACAACCTTG
SEQ ID NO: 766	CCAACTCACCGTGAGCCACTGGCCAACCTCTTCTTCTCC
SEQ ID NO: 767	CCAGGGCTCAGGATCCTCAGAGTTCACCTCCTTCTCTTA
SEQ ID NO: 768	GTCCACCTGCATGTTGAGCGTGTGATGGTATTCTAGGGG
SEQ ID NO: 769	GCGTGTCTGCACTGACAGTACTCCACTTCACTCTCAAAC
SEQ ID NO: 770	TGTCGGGTCTCCCTCACTCACATCCTTGTCCGCCCTCTTC
SEQ ID NO: 771	CTGCTGGCCAGCCCATTCATGCCATCCCCATCCCCAAA
SEQ ID NO: 772	GAATCCAGGCCCAACTCCAGGAGCATAAATGACTGGCC
SEQ ID NO: 773	TCTCAAATCCCTAATCCCGGCTGTTGGCCCTGTCCGCCTG

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 774	CCTGCCCCACGCGTGCAGCTGCTAAGCCCTCCCAATCCTG
SEQ ID NO: 775	CCCAGACACCCAGGGGACCCCTGAGATTCTGTCTGACCTCC
SEQ ID NO: 776	CTTCCCCAAGTCGCTCCTCTTACAAAGGCCCCACGGTC
SEQ ID NO: 777	CCTCTGGGTGCCAGGAGGCCTCTTGCCATGGGTGTCCTTC
SEQ ID NO: 778	CTGCCTTGTCTCTACCCACTGTGCTCTCCCTAGGACCAGG
SEQ ID NO: 779	GGCGAGGGGGAGGTCTGCAGCTGCTCGCGTGGGTGCC
SEQ ID NO: 780	TGCGCTCGATCTCATCCTTCAGTTCGTAGCCACCTGGGG
SEQ ID NO: 781	TCACCTGCTTCACAGGCGGGCTCCTGCCACTTGTGAA
SEQ ID NO: 782	CTCGCTTCTTCCGCTGTCCATCCAGGGGCGCAGGCAGCGG
SEQ ID NO: 783	CCCATGCCCTACCGGACCCCCAGGGCCCTCACCTGCGGCC
SEQ ID NO: 784	AGTCGGCTGGGAGGAGACGCCGGCTTCTCCCTCCATGA
SEQ ID NO: 785	ATCTTGCGGTACCTGGGACGGGTGGGTGGGCGCGCCAG
SEQ ID NO: 786	TGGCCTGCTTCCGGATCTCCGTGAGCCACAGCCGCTCCT
SEQ ID NO: 787	GGAGGGCGCTCTGGGAGTCTGACCTCTCCGAAGCTCATA
SEQ ID NO: 788	AGGAGGCAGAGGGCGGTGGCGGCTGGCTGGCTGTGGGTT
SEQ ID NO: 789	AGACATGAGCCAGGGCCACAGGACGAGAGGAGGGGGCGTG
SEQ ID NO: 790	CCAAGGGCCGCGAGGTCGCTTGGGGCTGAATGGATGGA
SEQ ID NO: 791	GATGGGAAGCCGCGGGGCTCTAAGCAGCGGAGACACAGG
SEQ ID NO: 792	GGAGCCTCTGGGCAGGGAGGAACCGGCCAAGGAGCCCGGG
SEQ ID NO: 793	GGCGGGGCCACAGGACGGGCGGCGTGCAGCAGGGCACT
SEQ ID NO: 794	CTGCAGGACCAAGGGATGACGCTGGGATAACAGAGGAGA
SEQ ID NO: 795	CAGAACAGGTTAATAGGATGAGGTGGCCTCTGAGTTCGG
SEQ ID NO: 796	CCATTCCTTCTTACTCGTGTGGGTGCGGGGATGTCAGGA
SEQ ID NO: 797	GGCCCGGTCCCAGCACTGCTCTGTGAGCTCAGAGTTGGGA
SEQ ID NO: 798	TGGGGGCCACACACGCGGGGATGCCGGGAGCCTGAGA
SEQ ID NO: 799	CACGGGCACCTGCTCCGGTACCCACTCGGCCCGGTGAGG
SEQ ID NO: 800	CTCCACCAGCCGGAAGCCAGCGGTACCAGCCGGCCGGT
SEQ ID NO: 801	AGGCGTCTCTCTCGATCTAGGGGAAGAGGAGGCCCTTG
SEQ ID NO: 802	ACTTGCCAGGTGGCCAGGCTGAATCCAGGTCTCTCTG
SEQ ID NO: 803	TGGCCTCGTTTACCTGTGTCTGCCGCACACGCCCACTGCC
SEQ ID NO: 804	GTCTGGCCCATACCTGCAGCGTCTTGGAGATCCTGGCCTT
SEQ ID NO: 805	GCTCCCCCACCTTGTGTCCCTCGGTCCCCAGCCCCACT
SEQ ID NO: 806	TGCAGGTTCCGCTGTGGGAGGACAGGAGGCTGCGATCT
SEQ ID NO: 807	TCGCGGATGGTGGACTTCCCGCCATATACGACGCTCTGCT
SEQ ID NO: 808	AGTGGGGTGAAGGCCACGCTGGAGGCCGTGCCGAGGAGC
SEQ ID NO: 809	CGGCTGCTGAGCCTAACCACTCCTGGGCTTCTTTCCAGC
SEQ ID NO: 810	GCTCATGGTATCCCTACCGCAGGCAATCTGTGGACAGCAC
SEQ ID NO: 811	CTGAATGTCACCTGAAGGTCACAGAAGCTACTCACAGGG

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 812	TTAAGTGTTCCTCAATATGAGATTAGCTGGAGCCGCCTAAT
SEQ ID NO: 813	GAAGATCCATCTGTGGAAGCCAGAGGACTAGTGGGAAAC
SEQ ID NO: 814	CCCCACAGGATCTGACACACAACCTAGGTTGTCAGCCA
SEQ ID NO: 815	GCCCAGCTTCCCAAGTCTGCCTGGACACCGCCCCATGGA
SEQ ID NO: 816	AATCACCTTCATGCTTAAACACTCACACTGATTCCAGC
SEQ ID NO: 817	CCTCTTGGGGACCTGGGTGACCTTACTCACCTCATGGCT
SEQ ID NO: 818	GTTGCTGTGGACAGGCTTGGAGCCGTTTTTGGCTGGAGAC
SEQ ID NO: 819	GGAGGGTAGGTGGCGGCACAGCTGGGACTGAGGGTGC
SEQ ID NO: 820	GCCAGGAGTGGTGTCTAAGGCAGAGGCAGCAGCGGGGGG
SEQ ID NO: 821	CAGGGCACTTGGGGTGTGCGGGGGCGGGACCCATTG
SEQ ID NO: 822	GGTGCCCGAGTTGTGGCTGGGAGCTGGACTGGCCTTGGGG
SEQ ID NO: 823	CTGCTTGCCAGCCCTCCACCGCACTGCTGTTACTACTG
SEQ ID NO: 824	GCCCCCACCCTGCTCCTCCTCACTCACTGGTGGCGCCA
SEQ ID NO: 825	CGGGCTGTCTGCCACAACCTGAGCTGTAACCTGGGAACAAA
SEQ ID NO: 826	GCTGGCATTGTTGCCCCACTGCTGCTCAAAGCCACCTCT
SEQ ID NO: 827	AGGTGGGTTGTGGGGCCGGAAGGGGGCCCAAGGCCTGG
SEQ ID NO: 828	TCCAACCCTGCCGATGGCCGAGACACTCACGAGGTGCTG
SEQ ID NO: 829	GGGGGTGAGGCGCTGCGCCTCTCTGTTTCAAAGGCTGC
SEQ ID NO: 830	ATTCCAGCAGCAAGGGCGGGGGTTTCCAGAACCCACCGAT
SEQ ID NO: 831	GGGGGTGTAACACCCGAGGGAGATGGAGGATAGCGCTTGG
SEQ ID NO: 832	CAAAGCAGGGAGGCTGATGTAGTTTCTTCTGCTGAAAGAA
SEQ ID NO: 833	CTTCCACTTAGATGAGAACGTATTTTAGAATGTTCTGAAG
SEQ ID NO: 834	TAACAGAAATGGGAGGAAAGGGTATGGGGCTCTTGAGAA
SEQ ID NO: 835	AAACAGTGACCTCCGGTGGCAGTCAATTGGCCTCAGGCA
SEQ ID NO: 836	GCAGAGGAATAAGGACTTCGGGACAATTCACCTTGAAAAG
SEQ ID NO: 837	GACCCAGTGGAAATGGTCTGAGCTAAGATTTGAAGGAGTGG
SEQ ID NO: 838	TGCACACTGATCTTCTTAGGGCATTCTTCGGGAAACAGG
SEQ ID NO: 839	GGCTCAGGATGAACAGCAACAGGGGTTGGGATGATCACTG
SEQ ID NO: 840	GATCATGGAGATGTGATCTAGGGAAACAAAGCCAGAGAAGG
SEQ ID NO: 841	AGGCATTCCCACGGTGTGAGGTCAGATTGGGCAGGGCCTA
SEQ ID NO: 842	AGAGCCAGCACTTGCTGTCCACACATACTAGATCAGTCT
SEQ ID NO: 843	TGGACAACCCCTCCACACCCAGAGCTGTGGAAGGGGAG
SEQ ID NO: 844	CACCTAGATGCTGACCAAGGCCCTCCCATGCTGCTGGAG
SEQ ID NO: 845	ATAAAGCCTTCATCTCCAGACCCCGCCCTTGCCCTGTT
SEQ ID NO: 846	AGGTGGTGAGTTTGGGGCTGGGGGGCCTCCCTGAGGAGCC
SEQ ID NO: 847	GAGAGAACCAGGTCCACATGCTGACACAGGTGTCCACGG
SEQ ID NO: 848	ATCCCCCAATCTCACCAGTGCACCCACAGACAAGGCGA
SEQ ID NO: 849	AAGGGCTTCAGCATAAGAGTCAGAACCCGCCCCCTTCTCT

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 850	TGTGGGCTGAAGGGACGAGGCTGGGGCACTGGGTGGGAGG
SEQ ID NO: 851	TTGCAATGTGGAAGAGTCAGGGGCACATTGTCTGGGCTGA
SEQ ID NO: 852	TAAGTGGGAGGGAGCGGGACCTAGTGTGGGCATGAGGAC
SEQ ID NO: 853	GGAGCAGGGATTTGGCTGGGCAATGGAGAGAAAGGTCTGA
SEQ ID NO: 854	ACACAGAGATGCCAGGAACCTGTCTTTAGTAAAGCAGC
SEQ ID NO: 855	TGGAGAGAGGTCCTTGAAGGTTTTGAACCCATAAAGAG
SEQ ID NO: 856	TCAGGAGGCAGCCAGTGATAGGGTCCAAGGAACCAGTGG
SEQ ID NO: 857	ACAGTCTACTGACTTTTCCTATTCAGCTGTGAGCATTCAA
SEQ ID NO: 858	CTGTCCCCTGGACCTTGACACCTGGCTCCCCAACCCCTGC
SEQ ID NO: 859	AGGAAACCCAGATTCCACCAGACACTTCCTTCTTCCCCC
SEQ ID NO: 860	GGCTATCTGGCCTGAGACAACAAATGCTGCCTCCCACCT
SEQ ID NO: 861	GTCTGGCACTGGACTTTCAGAACTCCTCCTTCCCTGACT
SEQ ID NO: 862	TTGCCCCAGACCCGTCATTC AATGGCTAGCTTTTTCCATG
SEQ ID NO: 863	AAAAACACGAGCACCCCCAACACAACGGCCAGTCTCTG
SEQ ID NO: 864	TTAACCTTGGACATGGTAAACCATCCAAAACCTTCCCTC
SEQ ID NO: 865	AGCAACTAAACCTCTCCACTGGGCACTTATCCTTGGTTTC
SEQ ID NO: 866	GAACCTCTTATTCTCTTAGAACCCACAGCTGCCACCACAG
SEQ ID NO: 867	TCCCTTCTCCAGTGTAAGACCCCAAATCACTCCAATGA
SEQ ID NO: 868	CAACCCCAACCCGATGCCTGCTTCAGATGTTTCCCATGT
SEQ ID NO: 869	CATAAACCTGGCTCCTAAAGGCTAAATATTTGTGGAGA
SEQ ID NO: 870	CTGCTGACCTGCCCTCCAGGTCAGAAATCATCCTCATGCA
SEQ ID NO: 871	TGTTCTCCAGACCTGTGCACTCTATCTGTGCAACAGAGAT
SEQ ID NO: 872	CGTGCAGCAAACAATGTGGAATCCAATAACCCCCACTC
SEQ ID NO: 873	AAATATGAGTCTCCCAAAGTCCCTAGCATTTCAAAATCC
SEQ ID NO: 874	CATCATAAAAAGATCTTGTGGTCCACAGATCCTCTAGCCC
SEQ ID NO: 875	CTCCCAACCCAGAATCCAGCTCCACAGATACATTGCTACT
SEQ ID NO: 876	CACTCTGAGACCAGAACTAGAACTTTTATTCTCATGCT
SEQ ID NO: 877	CACCAGCACTCAGGAGATTGTGAGACTCCCTGATCCCTGC
SEQ ID NO: 878	TGCCTAGATCCTTTGCACTCCAAGACCCAGTGTGCCCTAA
SEQ ID NO: 879	GGGGGTGGGTACGATCCCCGATTCTTCATACAAAGCCTCA
SEQ ID NO: 880	GGACAAAGGCAGAGGAGACACGCCCAGGATGAAACAGAAA
SEQ ID NO: 881	TGGATGCACCAGGCCCTGTAGCTCATGGAGACTTCATCTA
SEQ ID NO: 882	GGGAGAGCTAGCACTTGCTGTCTGCAATTACTAGATCAC
SEQ ID NO: 883	GGCTGGACAACCCCTCCACACCCAGAGCTGTGGAAGGG
SEQ ID NO: 884	TGGCACCCAGAGGCTGACCAAGGCCCTCCCATGCTGCTG
SEQ ID NO: 885	CCTATAAAAACCTTCATTCCCCAGGACTCCGCCCTGCCCT
SEQ ID NO: 886	TGCAGGTGGTAAGCTTGGGGCTGGGGAGCCTCCCCAGGA
SEQ ID NO: 887	AGGAAGACAACCGGACCCACATGGTGACACAGCTCTCCG

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 888	CAACCATGGCCCTCTCACCAATCCACGTCACGGACAGGG
SEQ ID NO: 889	TCAGCTTGACAGTCAGGGCTGGCTCCCTCTCTGCATCCC
SEQ ID NO: 890	TCCCTGTCTGGGCTGGGTGCTGGGTTGGGGGGAAAGAG
SEQ ID NO: 891	TGTGGGAGTGAGGACTGTTGCAATATGGAGGGGCTGGGGG
SEQ ID NO: 892	GGGAGAAAAGTTCTGGGGTAAGTGGGAGGGAGCGGGACCT
SEQ ID NO: 893	TGTGGGGCTCAAACCTCCAAGGACCTCTCTCAATGCCA
SEQ ID NO: 894	TGCCAACCCCTATCCCAGAGACCTTGATGCTTGGCCTCCC
SEQ ID NO: 895	TCTTGCCCTAGGATACCCAGATGCCAACCCAGACACCTCCT
SEQ ID NO: 896	TTCCTAGCCAGGCTATCTGGCCTGAGACAACAATGGGTC
SEQ ID NO: 897	TCTTAGCCCCAGACTCTTCATTCAGTGGCCACATTTTCC
SEQ ID NO: 898	AGGAAAAACATGAGCATCCCCAGCCACAACCTGCCAGCTCT
SEQ ID NO: 899	CCCCCTCAGAGTTACTGACAAACAGGTGGGCACTGAGACT
SEQ ID NO: 900	TGGAAAGTTAGCTTATTTGTTTGCAAGTCAGTAAAATGTC
SEQ ID NO: 901	GACTCAGGAGTCTCATGGACTCTGCCAGCATTCAAAAAC
SEQ ID NO: 902	ATGCTGTCTGCTAAGCTGTGAGCAGTAAAAGCCTTTGCCT
SEQ ID NO: 903	GATTTGGGGGGGCAAGGTGTAATAATGTGAACATGAACC
SEQ ID NO: 904	GTGTGCACAGCATCCACCTAGACTGCTCTGGTCACCCCTAC
SEQ ID NO: 905	AGGATTCCTAATCTCAGGTTTCTCACCCAGTGGCACAACC
SEQ ID NO: 906	CAAAGGCTGAGCAGGTTTGCAAGTTGTCCCAGTATAAGAT
SEQ ID NO: 907	GTC AAGGACAATCGATACAATATGTTCTCCAGAGTAGGT
SEQ ID NO: 908	GCAAGATGATATCTCTCTCAGATCCAGGCTTGCTTACTGT
SEQ ID NO: 909	TCTGTGTGCTTCTGAGCAAAGACAGCAACACCTTTTTTT
SEQ ID NO: 910	AACGTTGAGACTGTCTTGCAGACAAGGTTGGAAGGCTCTG
SEQ ID NO: 911	CATAAATAAGCAGGATGTGACAGAAGAAGTATTTAATGGT
SEQ ID NO: 912	GCTGCCAGACACAGTCGATCGGGACCTAGAACCTTGGTTA
SEQ ID NO: 913	GGGATCCTGAGCGCTGCCTTATTCTGGGTTTGGCAGTGGA
SEQ ID NO: 914	TCACTCAAACCCAGAAGTTCTGATCCCCAGCCATGCCCTT
SEQ ID NO: 915	AGCCTCTTCCCTTTGAAATTC AAGAGGGTGGACCCACT
SEQ ID NO: 916	GGAGCTGGGACCTTACCAGTCTCCTCCCTCATTGACCTAA
SEQ ID NO: 917	GAGGATATGAGATTCTTAGGCCATTCCACATCAGTACCT
SEQ ID NO: 918	TACCCAGAACTCTACCCCTCAGGATTCAGCACCTTCTTC
SEQ ID NO: 919	GCCTTGCCCTTCAGGGGCCAAAGAGCCTTAAGCCACAAA
SEQ ID NO: 920	ATCCCATTAATAACCCCAAACCTGGACCTAATGGTTC
SEQ ID NO: 921	AATGGGCAACCCTCGATCCTCAGACTCTTGAGGAATCAAG
SEQ ID NO: 922	GATACCCCTCAAGTGGAGTAAGGATTAGGTGGCAAGATGGA
SEQ ID NO: 923	GTGCTTGCCAGGGGCACCTTCATGGAGCTAGAAGGGCTG
SEQ ID NO: 924	GATGACACCC AAGGCTCTGGGGCATCTTTCATGCTCAGA
SEQ ID NO: 925	TGCTGGCCACACCCCTCAGAGTGTGGATGCTGGATGATGAG

TABLE 1-continued

Exemplary Probe Nucleotide Sequences	
SEQ ID NO	Nucleotide Sequence
SEQ ID NO: 926	GAGGCACGCTGCAGGGATAGTCACAGCAACATGACGTCAT
SEQ ID NO: 927	AGAGGAGGATGTCGGCAGCTCTACGGTTGGCAGGTGGCTG
SEQ ID NO: 928	GACACTAGGCCTCAGCCTGGCACCATGCAGGCCACTCCCA
SEQ ID NO: 929	ACTTTTGAGTCCTGGATCCCTATGATTCCAGGCTCCCTGT
SEQ ID NO: 930	CCTTGAGATTTTCATGGATGGTGACATATGGCCATTCTCTA
SEQ ID NO: 931	AAAACCCATAAGTTCAGGTCCTGTGCCCTCCACCCAGAA
SEQ ID NO: 932	TCGTATCTGGGAGACTCACTTGGGAGAGCAATAGACTTGG
SEQ ID NO: 933	TACAAGATGTGGTGGAGATAAGGCTGATGCTGGCACAGTG
SEQ ID NO: 934	GTACACACCATGGTGTTCATCAGGGCCCTGGGTAGTCCCT
SEQ ID NO: 935	GCTGTGACCTCACAGGAGTCCGTGCCTCCACCCCTACTC

A nucleic acid probe may be a non-labeled probe, or a probe that does not contain a detectable moiety. A non-labeled probe may further interact with a labeled probe (e.g., a labeled nucleic acid probe). A non-labeled probe may hybridize with a labeled nucleic acid probe. A non-labeled probe may also interact with a labeled polypeptide probe. The labeled polypeptide probe may be a protein that recognizes a sequence within the non-labeled probe. A labeled probe may include a nucleic acid portion and a polypeptide tag portion and the polypeptide tag portion may further interact with a molecule comprising a detectable moiety. For example, a non-labeled probe may be a nucleic acid probe comprising a streptavidin which may interact with a biotinylated molecule comprising a detectable moiety.

A nucleic acid probe may comprise about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% sequence specificity or sequence complementarity to a target site of a regulatory element. A nucleic acid probe may comprise about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% sequence specificity or sequence complementarity to a target nucleic acid sequence. The hybridization may be a high stringent hybridization condition.

A nucleic acid probe may hybridize with a genomic sequence that is present in low or single copy numbers (e.g., genomic sequences that are not repetitive elements). As used herein, repetitive element refers to a DNA sequence that is present in many identical or similar copies in the genome. Repetitive elements are not intended to refer to a DNA sequence that is present on each copy of the same chromosome a DNA sequence that is present only once, but is found on both copies of chromosome 11 would not be considered a repetitive element, and would be considered a sequence that is present in the genome as one copy). The genome may consist of three broad sequence components: single copy or at least very low copy number DNA (approximately 60% of the human genome); moderately, repetitive elements (approximately 30% of the human genome); and highly repetitive elements (approximately 10% of the human genome). For a review, see Human Molecular Genetics, Chapter 7 (1999), John Wiley & Sons, Inc.

A nucleic acid probe may have reduced off-target interaction. For example, "off-target" or "off-target interaction"

may refer to an instance in which a nucleic acid probe against a given target hybridizes or interact with another target site (e.g., a different DNA sequence, RNA sequence, or a cellular protein or other moiety).

A nucleic acid probe may further be cross-linked to a target site of a regulatory element. For example, the nucleic acid probe may be cross-linked by a photo-crosslinking means such as UV or by a chemical cross-linking means such as by formaldehyde, or through a reactive group within the nucleic acid probe. Reactive group may include sulfhydryl-reactive linkers such as bismaleimido-hexane (BMH), and the like.

A nucleic acid probe may include natural or unnatural nucleotide analogues or bases or a combination thereof. The unnatural nucleotide analogues or bases may comprise modifications at one or more of ribose moiety, phosphate moiety, nucleoside moiety, or a combination thereof. The unnatural nucleotide analogues or bases may comprise 2'-O-methyl, 2'-O-methoxyethyl (2'-O-MOE), 2'-O-aminopropyl, 2'-deoxy, T-deoxy-2'-fluoro, 2'-O-aminopropyl (2'-O-AP), 2'-O-dimethylaminoethyl (2'-O-DMAOE), 2'-O-dimethylaminopropyl (2'-O-DMAP), T-O-dimethylaminoethoxyethyl (2'-O-DMAEOE), or 2'-O-N-methylacetamido (2'-O-NMA) modified, locked nucleic acid (LNA), ethylene nucleic acid (ENA), peptide nucleic acid (PNA), 5'-anhydrohexitol nucleic acids (HNA), morpholino, methylphosphonate nucleotides, thiolphosphonate nucleotides, or 2'-fluoro N3-P5'-phosphoramidites. The nucleic acid probes may further comprise one or more abasic sites. The abasic site may further be functionalized with a detectable moiety.

A nucleic acid probe may comprise a Transcription Activator-Like Effector (TALE) sequence. A TALE may comprise a DNA-binding module which includes a variable number of about 33-35 amino acid residue repeats. Each amino acid repeat recognizes one base pair through two adjacent amino acids (such as at amino acid positions 12 and 13 of the repeat). As such, the amino acid repeat may also be referred to as repeat-variable diresidue (RVD).

A TALE probe described herein may comprise between about 1 to about 50 TALE repeat modules. A TALE probe described herein may comprise between about 5 and about 45, between about 8 and about 45, between about 10 and about 40, between about 12 and about 35, between about 15

and about 30, between about 20 and about 30, between about 8 and about 40, between about 8 and about 35, between about 8 and about 30, between about 10 and about 35, between about 10 and about 30, between about 10 and about 25, between about 10 and about 20, or between about 15 and about 25 TALE effector repeat modules.

A TALE probe described herein may comprise about 1, about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36, about 37, about 38, about 39, about 40, about 45, or about 50 TALE repeat modules. A TALE probe described herein may comprise about 5 TALE repeat modules. A TALE probe described herein may comprise about 10 TALE repeat modules. A TALE probe described herein may comprise about 11 TALE repeat modules. A TALE probe described herein may comprise about 12 TALE repeat modules. A TALE probe described herein may comprise about 13 TALE repeat modules. A TALE probe described herein may comprise about 14 TALE repeat modules. A TALE probe described herein may comprise about 15 TALE repeat modules. A TALE probe described herein may comprise about 16 TALE repeat modules. A TALE probe described herein may comprise about 17 TALE repeat modules. A TALE probe described herein may comprise about 18 TALE repeat modules. A TALE probe described herein may comprise about 19 TALE repeat modules. A TALE probe described herein may comprise about 20 TALE repeat modules. A TALE probe described herein may comprise about 21 TALE repeat modules. A TALE probe described herein may comprise about 22 TALE repeat modules. A TALE probe described herein may comprise about 23 TALE repeat modules. A TALE probe described herein may comprise about 24 TALE repeat modules. A TALE probe described herein may comprise about 25 TALE repeat modules. A TALE probe described herein may comprise about 26 TALE repeat modules. A TALE probe described herein may comprise about 27 TALE repeat modules. A TALE probe described herein may comprise about 28 TALE repeat modules. A TALE probe described herein may comprise about 29 TALE repeat modules. A TALE probe described herein may comprise about 30 TALE repeat modules. A TALE probe described herein may comprise about 35 TALE repeat modules. A TALE probe described herein may comprise about 40 TALE repeat modules. A TALE probe described herein may comprise about 45 TALE repeat modules. A TALE probe described herein may comprise about 50 TALE repeat modules.

A TAL effector repeat module may be a wild-type TALE DNA-binding module or a modified TALE DNA-binding repeat module enhanced for specific recognition of a nucleotide. A TALE probe described herein may comprise one or more wild-type TALE DNA-binding module. A TALE probe described herein may comprise one or more modified TAL effector DNA-binding repeat module enhanced for specific recognition of a nucleotide. A modified TALE DNA-binding repeat module may comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more mutations that may enhance the repeat module for specific recognition of a nucleic acid sequence (e.g., a target sequence). In some cases, a modified TALE DNA-binding repeat module is modified at amino acid position 2, 3, 4, 11, 12, 13, 21, 23, 24, 25, 26, 27, 28, 30, 31,

32, 33, 34, or 35. In some cases, a modified TALE DNA-binding repeat module is modified at amino acid positions 12 or 13.

A TALE repeat module may be a repeat module-like domain or RVD-like domain. A RVD-like domain has a sequence different from naturally occurring polynucleotide repeat module comprising RVD (RVD domain) but have a similar function and/or global structure. Non-limiting examples of RVD-like domains include protein domains selected from Puf RNA binding protein or Ankyrin superfamily.

A TALE repeat module may comprise a RVD domain of TABLE 2. A TALE probe described herein may comprise one or more RVD domains selected from TABLE 2. Sometimes, A TALE probe described herein may comprise up to 1, up to 2, up to 3, up to 4, up to 5, up to 6, up to 7, up to 8, up to 9, up to 10, up to 11, up to 12, up to 13, up to 14, up to 15, up to 16, up to 17, up to 18, up to 19, up to 20, up to 21, up to 22, up to 23, up to 24, up to 25, up to 26, up to 27, up to 28, up to 29, up to 30, up to 31, up to 32, up to 33, up to 34, up to 35, up to 36, up to 37, up to 38, up to 39, up to 40, up to 45, up to 50, up to 60, up to 70, up to 80, up to 90, or up to 100 RVD domains selected from TABLE 2.

TABLE 2

RVD	Nucleotide
HD	C
NG	T
NI	A
NN	G > A
NS	G, A > C > T
NH	G
N*	T > C >> G, A
NP	T > A, C
HG	T
H*	T
IG	T
HA	C
ND	C
NK	G
HI	C
HN	G > A
NT	G > A
NA	G
SN	G or A
SH	G
YG	T
IS	—

\*Denotes a gap in the repeat sequence corresponding to a lack of an amino acid residue at the second position of the RVD.

An RVD domain may recognize or interact with one nucleotide. An RVD domain may recognize or interact with more than one nucleotide. The efficiency of a RVD domain at recognizing a nucleotide is ranked as “strong”, “intermediate” or “weak”. The ranking may be according to a ranking described in Streubel et al., “TAL effector RVD specificities and efficiencies,” *Nature Biotechnology* 30(7): 593-595 (2012). The ranking of RVD may be as illustrated in TABLE 3, based on the ranking provided in Streubel et al. *Nature Biotechnology* 30(7): 593-595 (2012).

TABLE 3

RVD	Nucleotide	Efficiency
HD	C	strong
NG	T	weak
NI	A	weak
NN	G > A	Strong (G), intermediate (A)
NS	G, A > C > T	intermediate

TABLE 3-continued

RVD	Nucleotide	Efficiency
NH	G	intermediate
N*	T > C >> G, A	weak
NP	T > A, C	intermediate
NK	G	weak
HN	G > A	intermediate
NT	G > A	intermediate
SN	G or A	Weak
SH	G	Weak
IS	—	weak

\*Denotes a gap in the repeat sequence corresponding to a lack of an amino acid residue at the second position of the RVD.

A TALE DNA-binding domain may further comprise a C-terminal truncated TALE DNA-binding repeat module. A C-terminal truncated TALE DNA-binding repeat module may be between about 18 and about 40 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be between about 20 and about 40, between about 22 and about 38, between about 24 and about 35, between about 28 and about 32, between about 25 and about 40, between about 25 and about 38, between about 25 and about 30, between about 28 and about 40, or between about 28 and about 35 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, at least 30, at least 31, at least 32, at least 33, at least 34, at least 35, at least 36, at least 37, at least 38, at least 39, or more residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 18, about 19, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36 about 37, about 38, about 39, or about 40 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 18 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 19 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 20 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 21 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 22 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 23 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 24 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 25 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 26 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 27 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 28 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 29 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 30 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 31 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 32 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 33 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 34 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 35 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 36 resi-

dues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 37 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 38 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 39 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be about 40 residues in length. A C-terminal truncated TALE DNA-binding repeat module may be a RVD domain of TABLE 2.

A TALE DNA-binding domain may further comprise an N-terminal cap. An N-terminal cap may be a polypeptide portion flanking the DNA-binding repeat module. An N-terminal cap may be any length and may comprise from about 0 to about 136 amino acid residues in length. An N-terminal cap may be about 5, about 10, about 15, about 20, about 25, about 30, about 35, about 40, about 45, about 50, about 60, about 70, about 80, about 90, about 100, about 110, about 120, or about 130 amino acid residues in length. An N-terminal cap may modulate structural stability of the DNA-binding repeat modules. An N-terminal cap may modulate nonspecific interactions. An N-terminal cap may decrease nonspecific interaction. An N-terminal cap may reduce off-target effect. As used here, off-target effect refers to the interaction of a TALE protein with a sequence that is not the target sequence of interest. An N-terminal cap may further comprise a wild-type N-terminal cap sequence of a TALE protein or may comprise a modified N-terminal cap sequence.

A TALE DNA-binding domain may further comprise a C-terminal cap sequence. A C-terminal cap sequence may be a polypeptide portion flanking the C-terminal truncated TALE DNA-binding repeat module. A C-terminal cap may be any length and may comprise from about 0 to about 278 amino acid residues in length. A C-terminal cap may be about 5, about 10, about 15, about 20, about 25, about 30, about 35, about 40, about 45, about 50, about 60, about 80, about 100, about 150, about 200, or about 250 amino acid residues in length. A C-terminal cap may further comprise a wild-type C-terminal cap sequence of a TALE protein, or may comprise a modified C-terminal cap sequence.

A nuclease domain may be linked to a TALE DNA-binding domain either directly or through a linker. A linker may be between about 1 and about 50 amino acid residues in length. A linker may be from about 5 to about 45, from about 5 to about 40, from about 5 to about 35, from about 5 to about 30, from about 5 to about 25, from about 5 to about 20, from about 5 to about 15, from about 10 to about 40, from about 10 to about 35, from about 10 to about 30, from about 10 to about 25, from about 10 to about 20, from about 12 to about 40, from about 12 to about 35, from about 12 to about 30, from about 12 to about 25, from about 12 to about 20, from about 14 to about 40, from about 14 to about 35, from about 14 to about 30, from about 14 to about 25, from about 14 to about 20, from about 14 to about 16, from about 15 to about 40, from about 15 to about 35, from about 15 to about 30, from about 15 to about 25, from about 15 to about 20, from about 15 to about 18, from about 18 to about 40, from about 18 to about 35, from about 18 to about 30, from about 18 to about 25, from about 18 to about 24, from about 20 to about 40, from about 20 to about 35, from about 20 to about 30, or from about 25 to about 30 amino acid residues in length.

A linker for linking a nuclease domain to a TALE DNA-binding domain may be about 1, about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about

23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 35, about 40, about 45, or about 50 amino acid residues in length. A linker may be about 10 amino acid residues in length. A linker may be about 11 amino acid residues in length. A linker may be about 12 amino acid residues in length. A linker may be about 13 amino acid residues in length. A linker may be about 14 amino acid residues in length. A linker may be about 15 amino acid residues in length. A linker may be about 16 amino acid residues in length. A linker may be about 17 amino acid residues in length. A linker may be about 18 amino acid residues in length. A linker may be about 19 amino acid residues in length. A linker may be about 20 amino acid residues in length. A linker may be about 21 amino acid residues in length. A linker may be about 22 amino acid residues in length. A linker may be about 23 amino acid residues in length. A linker may be about 24 amino acid residues in length. A linker may be about 25 amino acid residues in length. A linker may be about 26 amino acid residues in length. A linker may be about 27 amino acid residues in length. A linker may be about 28 amino acid residues in length. A linker may be about 29 amino acid residues in length. A linker may be about 30 amino acid residues in length.

A TALE probe may be designed to recognize each strand of a double-stranded segment of DNA by engineering the TALE to include a sequence of repeat-variable diresidue subunits that may comprise about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36, about 37, about 38, about 39, or about 40 amino acid repeats capable of associating with specific DNA sequences, such that the detectable label of the TALE probe is located at the target nucleic acid sequence.

A nucleic acid probe may be a locked nucleic acid probe (such as a labeled locked nucleic acid probe), a labeled or unlabeled peptide nucleic acid (PNA) probe, a labeled or unlabeled oligonucleotide, an oligopaint, an ECHO probe, a molecular beacon probe, a padlock (or molecular inversion probe), a labeled or unlabeled toe-hold probe, a labeled TALE probe, a labeled ZFN probe, or a labeled CRISPR probe.

A nucleic acid probe may be a labeled or unlabeled locked nucleic acid probe or a labeled or unlabeled peptide nucleic acid probe. Locked nucleic acid probes and peptide nucleic acid probes are known to those of skill in the art and are described in Briones et al., *Anal Bioanal Chem* (2012) 402:3071-3089.

A nucleic acid probe may be a padlock (or molecular inversion probe). A padlock probe may be hybridized to a target regulatory element sequence in which the two ends may correspond to the target sequence. A padlock probe may be ligated together by a ligase (such as T4 ligase) when bound to the target sequence. An amplification (such as a rolling circle amplification or RCA) may be performed utilizing for example  $\Phi$ 29 polymerase, which may result in a single stranded DNA comprising multiple tandem copies of the target sequence.

A nucleic acid probe may be an oligopaint as described in U.S. Publication No. 2010/0304994; and in Beliveau, et al., "Versatile design and synthesis platform for visualizing genomes with oligopaint FISH probes," *PNAS* 109(52): 21301-21306 (2012). Oligopaint may refer to detectably labeled polynucleotides that have sequences complementary to an oligonucleotide sequence (such as a portion of a DNA sequence, like a particular chromosome or sub-chromosomal region of a particular chromosome). Oligopaints may

be generated from synthetic probes and arrays that are, optionally, computationally patterned (rather than using natural DNA sequences and/or chromosomes as a template).

A nucleic acid probe may be a labeled or unlabeled toe-hold probe. Toe-hold probes are known to those of skill in the art as described in Zhang et al., *Optimizing the Specificity of Nucleic Acid Hybridization*, *Nature Chemistry* 4: 208-214 (2012).

A nucleic acid probe may be a molecular beacon. Molecular beacons may be hairpin shaped molecules with an internally quenched fluorophore whose fluorescence is restored when they bind to a target nucleic acid sequence. Molecular beacons are known to those of skill in the art as described in Guo et al., *Anal. Bioanal. Chem.* (2012) 402: 3115-3125.

A nucleic acid probe may be an ECHO probe. ECHO probes may be sequence-specific, hybridization-sensitive, quencher-free fluorescent probes for RNA detection, which may be designed using the concept of fluorescence quenching caused by intramolecular excitonic interaction of fluorescent dyes. ECHO probes are known to those of skill in the art as described in Kubota et al., *PLoS ONE*, Vol. 5, Issue 9, e13003 (2010); or Okamoto, *Chem. Soc. Rev.*, 2011, 40, 5815-5828, Wang et al., *RNA* (2012), 18:166-175.

A probe may be a clustered regularly interspaced palindromic repeat (CRISPR) probe. The CRISPR system may use a Cas9 protein to recognize DNA sequences, in which the target specificity may be solely determined by a small guide (sg) RNA and a protospacer adjacent motif (PAM). Upon binding to target DNA, the Cas9-sgRNA complex may generate a DNA double-stranded break. For imaging applications, a Cas9 protein may be replaced with an endonuclease-deactivated Cas9 (dCas9) protein. For example, imaging a cell, such as by fluorescence in situ hybridization (FISH), may be achieved by synthesizing a dCas9 within the cell, synthesizing RNA within the cell to bind genomic DNA and to complex with the dCas9 forming a dCas9/RNA complex, labeling the dCas9/RNA complex, and imaging the labeled dCas9/RNA complex within the live cell bound to genomic DNA. The endonuclease-deactivated Cas9 may be synthesized in vivo by using an integrated construct, a transiently transfected construct, by injection into the cell of a syncytia of nuclei or via electroporation into cells and/or nuclei.

A probe may comprise an endonuclease-deactivated Cas9 (dCas9) protein as described in Chen et al., "Dynamic imaging of genomic loci in living human cells by an optimized CRISPR/Cas system," *Cell* 155(7): 1479-1491 (2013); or Ma et al., "Multicolor CRISPR labeling of chromosomal loci in human cells," *PNAS* 112(10): 3002-3007 (2015). The dCas9 protein may be further labeled with a detectable moiety.

The RNA of the Cas9/RNA complex may be synthesized in vivo by using an integrated construct, a transiently transfected construct, by injection into the cell of a syncytia of nuclei or via electroporation into cells and/or nuclei. The Cas9/RNA complex may be labeled by making a fusion protein that includes Cas9 and a reporter, by injection of RNA that has been attached to a reporter into the cell or by a syncytia of nuclei including RNA that has been attached to a reporter, by electroporation into cells or nuclei or by indirect labeling of the RNA by hybridization with a labeled secondary oligonucleotide. The label may be a conditional reporter, based on the binding of Cas9/RNA to the target nucleic acid. The label may be quenched and may then be activated upon the Cas9/RNA complex binding to the target nucleic acid.

A probe may be a transcription activator-like effector nuclease (TALEN) probe. TALENs are engineered restriction enzymes generated by fusing the TALE DNA binding domain to a FokI DNA cleavage domain. A FokI DNA cleavage domain may comprise an endonuclease-deactivated FokI domain. A nucleic acid probe may be a TALEN probe comprising an endonuclease-deactivated FokI domain.

A probe may be a zinc-finger nuclease (ZFN) probe. Similar to TALEN, a zinc-finger nuclease is an engineered restriction enzyme generated by fusing a zinc finger DNA-binding domain to a zinc finger nuclease. A zinc finger nuclease may comprise an endonuclease-deactivated zinc finger nuclease. A nucleic acid probe may be a ZFN probe comprising an endonuclease-deactivated zinc finger nuclease.

A probe disclosed herein may be a polypeptide probe. A polypeptide probe may include a protein or a binding fragment thereof that interacts with a target site (such as a nucleic acid target site or a protein target) of interest. A polypeptide probe may comprise a DNA-binding protein, a RNA-binding protein, a protein involved in the transcription/translation process or detects the transcription/translation process, a protein that may detect an open or relaxed portion of a chromatin, or a protein interacting partner of a product of a regulatory element.

A polypeptide probe may be a DNA-binding protein. The DNA-binding protein may be a transcription factor that modulates the transcription process, polymerases, or histones. A DNA-binding protein may comprise a zinc finger domain, a helix-turn-helix domain, a leucine zipper domain (such as a basic leucine zipper domain), a high mobility group box (HMG-box) domain, and the like. The DNA-binding protein may interact with a nucleic acid region in a sequence specific manner. The DNA-binding protein may interact with a nucleic acid region in a sequence non-specific manner. The DNA-binding protein may interact with single-stranded DNA. The DNA-binding protein may interact with double-stranded DNA. The DNA-binding protein probe may further comprise a detectable moiety.

A polypeptide probe may be a RNA-binding protein. The RNA-binding protein may participate in forming ribonucleoprotein complexes. The RNA-binding protein may modulate post-transcription such as in splicing, polyadenylation, mRNA stabilization, mRNA localization, or in translation. A RNA-binding protein may comprise a RNA recognition motif (RRM), dsRNA binding domain, zinc finger domain, K-Homology domain (KH domain), and the like. The RNA-binding protein may interact with single-stranded RNA. The RNA-binding protein may interact with double-stranded RNA. The RNA-binding protein probe may further comprise a detectable moiety.

A polypeptide probe may be a protein that may detect an open or relaxed portion of a chromatin. The polypeptide probe may be a modified enzyme that lacks cleavage activity. The modified enzyme may be an enzyme that recognizes DNA or RNA (double-stranded or single-stranded). Examples of modified enzymes may be obtained from oxidoreductases, transferases, hydrolases, lyases, isomerases, or ligases. A modified enzyme may be an endonuclease (such as a deactivated restriction endonuclease such as the TALEN or CRISPR probes described herein).

A polypeptide probe may be an antibody or binding fragment thereof. The antibody or binding fragment thereof may be a protein interacting partner of a product of a regulatory element. The antibody or binding fragment

thereof may comprise a humanized antibody or binding fragment thereof, murine antibody or binding fragment thereof, chimeric antibody or binding fragment thereof, monoclonal antibody or binding fragment thereof, monovalent Fab', divalent Fab2, F(ab)'3 fragments, single-chain variable fragment (scFv), bis-scFv, (scFv)2, diabody, minibody, nanobody, triabody, tetrabody, disulfide stabilized Fv protein (dsFv), single-domain antibody (sdAb), Ig NAR, camelid antibody or binding fragment thereof, or a chemically modified derivative thereof. The antibody or binding fragment thereof may further comprise a detectable moiety.

Multiple probes may be used together in a probe set to detect a nucleic acid sequence using Nano-FISH. The probe set may be designed for the detection of the target nucleic acid sequence. For example, the probe set may be optimized for probes based on GC content, 16mer base matches (for determining binding specificity of the probe), and their predicted melting temperature when hybridized. The 16mer base matches may have a total of 24 matches to the 16mer database. In some embodiments, probe sets with greater than 100 16-mer database matches may be discarded.

Exemplary probe nucleotide sequences are shown in TABLE 1 for probe sets for different target sequences. Some exemplary probe sequences may be target sequences located in the GREB1 promoter of chromosome 2, ER iDHS1 of chromosome 2, ER iDHS2 of chromosome 2, HBG1up of chromosome 11, HBG2 up of chromosome 11, HS1 of chromosome 11, HS2 of chromosome 11, HS3 of chromosome 11, HS4 of chromosome 11, HS5 of chromosome 11, HS1 Lflank of chromosome 11, HS1 2 flank of chromosome 11, HS2 3 flank of chromosome 11, HS3 4 flank of chromosome 11, HS4 5 flank of chromosome 11, HS5 Rflank of chromosome 11, CCND1 SNP of chromosome 11, CCND1 CTL of chromosome 11, the CCND1 promoter of chromosome 11, Chromosome 18 dead1 of chromosome 18, Chromosome 18 dead2 of chromosome 18, Chromosome dead3 of chromosome 18, CNOT promoter of chromosome 19, CNOT inter1 of chromosome 19, CNOT inter2 of chromosome 19, CNOT inter3 of chromosome 19, TSEN promoter of chromosome 19, KLK2 promoter of chromosome 19, KLK3 promoter of chromosome 19, or KLK eRNA of chromosome 19. GREB1 is gene that may be induced by estrogen stimulation of MCF-7 breast cancer cells. ER iDHS1 and ER iDHS2 are DHS that may be induced by estrogen stimulation of MCF-7 breast cancer cells. HBG1up and HBG2up are hemoglobin genes expressed in K562 erythroleukemia cells. HS1, HS2, HS3, HS4, and HS5 are hypersensitive sites in the beta-globin locus control region, and HS1 Lflank, HS2 3flank, HS3 4flank, HS4 5flank, HS5 Rflank are sequences in the intervening regions between HS1-HS5. CCND1 SNP is an enhancer for the CCND1 gene, CCND1 CTL is a control region adjacent to the CCND1 SNP, and the CCND1 promoter is the promoter region of the CCND1 gene. Chromosome 18 dead1, Chromosome 18 dead 2, and Chromosome 18 dead3 are non-hypersensitive regions of chromosome 18. The CNOT promoter is the promoter (active region) of CNOT. The TSEN promoter is the promoter (active region) of TSEN. The KLK2 promoter is the promoter KLK2. The KLK3 promoter is the promoter of KLK3. KLK eRNA is an enhancer for the KLK2 gene and/or the KLK3 gene, and which may also enhance RNA. For example, a probe set comprising at least nine different Q570 labeled probes selected from the group consisting of SEQ ID NO: 1-SEQ ID NO: 39 may be used to detect the GREB1 promoter in chromosome 2. A Q570 labeled probe set comprising probes with SEQ ID NO: 7-SEQ ID NO: 35 may be used to detect the GREB1 promoter in chromosome

2. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 40-SEQ ID NO: 72 may be used to detect the ER iDHS 1 in chromosome 2. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 73-SEQ ID NO: 104 may be used to detect the ER iDHS 2 in chromosome 2. A probe set comprising at least nine different Q570 labeled probes selected from the group consisting of SEQ ID NO: 105-SEQ ID NO: 134 may be used to detect the HBGlup in chromosome 11. A probe set comprising at least nine different Q570 labeled probes selected from the group consisting of SEQ ID NO: 135-SEQ ID NO: 164 may be used to detect the HBG2up in chromosome 11. A probe set comprising at least nine different Q570/670 labeled probes selected from the group consisting of SEQ ID NO: 165-SEQ ID NO: 194 may be used to detect HS1 in chromosome 11. A probe set comprising at least nine different Q570/670 labeled probes selected from the group consisting of SEQ ID NO: 195-SEQ ID NO: 224 may be used to detect HS2 in chromosome 11. A probe set comprising at least nine different Q570/670 labeled probes selected from the group consisting of SEQ ID NO: 225-SEQ ID NO: 254 may be used to detect HS3 in chromosome 11. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 255-SEQ ID NO: 298 may be used to detect HS4 in chromosome 11. A probe set comprising at least nine different Q570/670 labeled probes selected from the group consisting of SEQ ID NO: 299-SEQ ID NO: 340 may be used to detect HS5 in chromosome 11. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 341-SEQ ID NO: 370 may be used to detect HS1 Lflank in chromosome 11. A probe set comprising at least nine different Q570 labeled probes selected from the group consisting of SEQ ID NO: 371-SEQ ID NO: 400 may be used to detect HS1 2flank in chromosome 11. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 401-SEQ ID NO: 430 may be used to detect HS2 3flank in chromosome 11. A probe set comprising at least nine different Q570 labeled probes selected from the group consisting of SEQ ID NO: 431-SEQ ID NO: 460 may be used to detect HS3 4flank in chromosome 11. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 461-SEQ ID NO: 484 may be used to detect HS4 5flank in chromosome 11. A probe set comprising at least nine different Q570 labeled probes selected from the group consisting of SEQ ID NO: 485-SEQ ID NO: 514 may be used to detect HS5 Rflank in chromosome 11. A probe set comprising at least nine different Q570 labeled probes selected from the group consisting of SEQ ID NO: 515-SEQ ID NO: 544 may be used to detect CCND1 SNP in chromosome 11. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 545-SEQ ID NO: 564 may be used to detect CCND1 CTL in chromosome 11. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 565-SEQ ID NO: 598 may be used to detect the CCND1 promoter in chromosome 11. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 599-SEQ ID NO: 628 may be used to detect Chromosome 18 dead1 in chromosome 18. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 629-SEQ ID NO: 658 may be used to detect Chromosome 18 dead2 in chromosome 18. A

probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 659-SEQ ID NO: 688 may be used to detect Chromosome 18 dead3 in chromosome 18. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 689-SEQ ID NO: 718 may be used to detect the CNOT3 promoter in chromosome 19. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 719-SEQ ID NO: 748 may be used to detect the TSEN34 promoter in chromosome 19. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 749-SEQ ID NO: 778 may be used to detect CNOT3 inter1 in chromosome 19. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 779-SEQ ID NO: 808 may be used to detect CNOT3 inter2 in chromosome 19. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 809-SEQ ID NO: 838 may be used to detect CNOT3 inter3 in chromosome 19. A probe set comprising at least nine different Q570 labeled probes selected from the group consisting of SEQ ID NO: 839-SEQ ID NO: 868 may be used to detect the KLK2 promoter in chromosome 19. A probe set comprising at least nine different Q570 labeled probes selected from the group consisting of SEQ ID NO: 869-SEQ ID NO: 898 may be used to detect the KLK3 promoter in chromosome 19. A probe set comprising at least nine different Q670 labeled probes selected from the group consisting of SEQ ID NO: 899-SEQ ID NO: 935 may be used to detect KLK eRNA in chromosome 19.

#### Detectable Moieties

A detecting agent may comprise a detectable moiety. A detectable moiety may be a small molecule (such as a dye) or a macromolecule. A macromolecule may include polypeptides (such as proteins and/or protein fragments), nucleic acids, carbohydrates, lipids, macrocycles, polyphenols, and/or endogenous macromolecule complexes. A detectable moiety may be a small molecule. A detectable moiety may be a macromolecule.

A detectable moiety may include a moiety that is detectable by a colorimetric method or a fluorescent method. For example, a colorimetric method may be an assay which utilizes reagents that undergo a measurable color change in the presence of an analyte (such as an enzyme, an antibody, a compound, a hormone). Exemplary colorimetric method may include enzyme-mediated detection method such as tyramide signal amplification (TSA) which utilizes horseradish peroxidase (HRP) to generate a signal when digested by tyramide substrate and 3,3',5,5'-Tetramethylbenzidine (TMB) which generates a blue color upon oxidation to 3,3',5,5'-tetramethylbenzidine diamine in the presence of a peroxidase enzyme such as HRP. A detectable moiety described herein may include a moiety that is detectable by a colorimetric method.

A detectable moiety may also include a moiety that is detectable by a fluorescent method. Sometimes, the detectable moiety may be a fluorescent moiety. A fluorescent moiety may be a small molecule (such as a dye) or a fluorescently labeled macromolecule. A fluorescently labeled macromolecule may include a fluorescently labeled polypeptide (such as a labeled protein and/or a protein fragment), a fluorescently labeled nucleic acid molecule, a fluorescently labeled carbohydrate, a fluorescently labeled lipid, a fluorescently labeled macrocycle, a fluorescently labeled polyphenol, and/or a fluorescently labeled endog-

enous macromolecule complex (such as a primary antibody-secondary antibody complex).

A fluorescent small molecule may comprise rhodamine, rhodol, fluorescein, thiofluorescein, aminofluorescein, carboxyfluorescein, chlorofluorescein, methylfluorescein, sulfofluorescein, aminorhodol, carboxyrhodol, chlororhodol, methylrhodol, sulforhodol; aminorhodamine, carboxyrhodamine, chlororhodamine, methylrhodamine, sulforhodamine, thiorhodamine, cyanine, indocarbocyanine, oxacarbocyanine, thiocarbocyanine, merocyanine, cyanine 2, cyanine 3, cyanine 3.5, cyanine 5, cyanine 5.5, cyanine 7, oxadiazole derivatives, pyridyloxazole, nitrobenzoxadiazole, benzoxadiazole, pyren derivatives, cascade blue, oxazine derivatives, Nile red, Nile blue, cresyl violet, oxazine 170, acridine derivatives, proflavin, acridine orange, acridine yellow, arylmethine derivatives, auramine, crystal violet, malachite green, tetrapyrrole derivatives, porphyrin, phthalocyanine, bilirubin 1-dimethylaminonaphthyl-5-sulfonate, 1-anilino-8-naphthalene sulfonate, 2-p-touidinyln-6-naphthalene sulfonate, 3-phenyl-7-isocyanatocoumarin, N-(p-(2-benzoxazolyl)phenyl)maleimide, stilbenes, pyrenes, 6-FAM (Fluorescein), 6-FAM (NHS Ester), 5(6)-FAM, 5-FAM, Fluorescein dT, 5-TAMRA-cadavarine, 2-aminoacridone, HEX, JOE (NHS Ester), MAX, TET, ROX, TAMRA, TARMA™ (NHS Ester), TEX 615, ATTO™ 488, ATTO™ 532, ATTO™ 550, ATTO™ 565, ATTO™ Rho101, ATTO™ 590, ATTO™ 633, ATTO™ 647N, TYE™ 563, TYE™ 665, or TYE™ 705.

A fluorescent moiety may comprise Cy3, Cy5, Cy5.5, Cy7, Q570, Alexa488, Alexa555, Alexa594, Alexa647, Alexa680, Alexa 750, Alexa 790, Atto488, Atto532, Atto647N, TexasRed, CF610, Propidium iodide, Quasar 570 (Q570), Quasar 670 (Q670), IRDye700, IRDye800, Indocyanine green, Pacific Blue dye, Pacific Green dye, or Pacific Orange dye.

A fluorescent moiety may comprise a quantum dot (QD). Quantum dots may be a nanoscale semiconducting photoluminescent material, for example, as described in Alivisatos A. P., "Semiconductor clusters, nanocrystals, and quantum dots," *Science* 271(5251): 933-937 (1996).

Exemplary QDs may include, but are not limited to, CdS quantum dots, CdSe quantum dots, CdSe/CdS core/shell quantum dots, CdSe/ZnS core/shell quantum dots, CdTe quantum dots, PbS quantum dots, and/or PbSe quantum dots. As used herein, CdSe/ZnS may mean that a ZnS shell is coated on a CdSe core surface (a "core-shell" quantum dot). The shell materials of core-shell QDs may have a higher bandgap and passivate the core QDs surfaces, resulting in higher quantum yield and higher stability and wider applications than core QDs.

QDs may absorb a wide spectrum of light, and may be physically tuned with emission bandwidths in various wavelengths. See, e.g., Badolato, et al., *Science* 208:1158-61 (2005). For example, the emission bandwidth may be in the visible spectrum (from about 350 to about 750 nm), the ultraviolet-visible spectrum (from about 100 nm to about 750 nm), or in the near-infrared spectrum (from about 750 nm to about 2500 nm). QDs that emit energy in the visible range may include, but are not limited to, CdS, CdSe, CdTe, ZnSe, ZnTe, GaP, and GaAs. QDs that emit energy in the blue to near-ultraviolet range include, but are not limited to, ZnS and GaN. QDs that emit energy in the near-infrared range include, but are not limited to, InP, InAs, InSb, PbS, and PbSe.

The radius of a QD may be modulated to manipulate the emission bandwidth. For example, a radius of between about 5 and about 6 nm QD may emit wavelengths resulting in

emission colors such as orange or red. A radius of between about 2 and about 3 nm may emit wavelengths resulting in emission colors such as blue or green.

A QD may further form a QD microstructure, which encompasses one or more layers of QD. For example, each quantum dot containing layer may comprise a single type of quantum dot of a specific emission color. For example, each layer may be made of any material suitable for use that (a) allows excitation light to reach the quantum dot and allows fluorescence generated from the quantum dot to pass through the layer(s) for detection and (b) may be combined with a quantum dot to form a layer. Examples of materials that may be used to form layers containing quantum dots include, but are not limited to, inorganic, organic, or polymeric material, each with or without biodegradable properties, and combinations thereof. The layers may comprise silica-based compounds or polymers. Exemplary silica-based layers may include, but are not limited to, those comprising tetramethoxy silane or tetraethylorthosilicate. Exemplary polymer layers may include, but are not limited to, those comprising polystyrene, poly (methyl methacrylate), polyhydroxyalkanoate, polylactide, or co-polymers thereof.

The quantum dot further may comprise a spacer layer which serves as a barrier to prevent interactions between different QD layers, and may be made of any material suitable for use that (a) allows excitation light to reach the quantum dots in the quantum dot containing layer(s) below it and allows fluorescence generated from those quantum dots to pass through it and (b) may segregate the quantum dots in one layer from those in other layers. Examples of materials that may be used to form spacer layers are the same as for the quantum dot containing layers.

The materials used for the quantum dot containing and spacer layers may be the same or different. The same material may be used in the quantum dot containing layers and the spacer layers.

The quantum dot containing layers and the spacer layers within a given QD molecule may be any thickness and may be varied. For example, thicker QD-containing layers may allow for the loading of increased QDs in the shell, resulting in greater fluorescence intensity for that layer than for a thinner layer containing the same concentration of QDs. Thus, varying layer thickness may facilitate preparing QD-containing layer of various intensities, thereby generating spectrally distinct QD bar codes. In various instances, the QD-containing layers may be between 5 nm and 500 nm; 10 nm and 500 nm; 5 nm and 100 nm, and 10 nm and 100 nm. Those of skill in the art will understand that other methods for varying intensity also exist, for example, modifying concentrations of the same QD in one microstructure with a first unique barcode compared to a second QD microstructure with a different fluorescent barcode. The ability to vary the intensities for the same QD color allows for an increased number of distinct and distinguishable microstructures (e.g., spectrally distinct barcodes). The spacer layers may be greater than 10 nm, up to approximately 5 μm thick; the spacer layers may be greater than 10 nm, up to approximately 500 nm thick; the space layers may be greater than 10 nm, up to approximately 100 nm thick.

The quantum dot-containing and spacer layers may be arranged in any order. Examples include, but are not limited to, alternating QD-containing layers and spacer layers, or quantum dot containing layers separated by more than one spacer layer. Thus, a "spacer layer" may comprise a single layer, or may comprise two or more such spacer layers.

The QD microstructure may comprise any number of quantum dot containing layers suitable for use with the microstructure. For example, a microstructure described herein may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10, or more quantum dot-containing layers and an appropriate number of spacer layers based on the number of quantum dot-containing layers. Further, the number of quantum dot containing layers in a given microstructure may range from 1 to “m,” where “m” is the number of quantum dots that may be used.

A defined intensity level may refer to a known amount of quantum dots in each quantum dot containing layer, resulting in a known amount of fluorescent intensity generated from the QD containing layer upon appropriate stimulation. Since each QD containing layer has a defined intensity level, each microstructure may possess a defined ratio of fluorescence intensities generated from the various QD-containing layers upon stimulation. This defined ratio is referred to herein as a barcode. Thus, each type of microstructure with the same QD layers possesses a similar barcode that may be distinguished from microstructures with different QD layers.

Thus, each quantum dot containing layer may comprise a single type of quantum dot of a specific emission color and the layer is produced to possess a defined intensity level, based on the concentration of the QD in the layer. By varying the intensity levels of QDs (“n”) in different microstructures and using a variety of different quantum dots (“m”), the number of different unique barcodes (and thus the number of different unique microstructure populations that may be produced) is approximated by the equation,  $(n^m - 1)$  unique codes. This may provide the ability to generate a large number of different populations of microstructures each with its own unique barcode.

A set of QD-labeled probes may further generate a spectrally distinct barcode. For example, each probe with the set of QD-labeled probes may comprise a QD with a distinct excitation wavelength and the combination of the set may generate a distinct barcode. A set of spectrally distinct QD-labeled probes may be utilized to detect a regulatory element. As such, when detecting two or more regulatory elements, each regulatory element may be spectrally bar-coded.

A quantum dot provided herein may include QDot525, QDot 545, QDot 565, QDot 585, QDot 605, or QDot 655. A probe described herein may comprise a quantum dot. A probe described herein may comprise QDot525, QDot 545, QDot 565, QDot 585, QDot 605, or QDot 655. A probe described herein may comprise QDot525. A probe described herein may comprise QDot 545. A probe described herein may comprise QDot 565. A probe described herein may comprise QDot 585. A probe described herein may comprise QDot 605. A probe described herein may comprise QDot 655.

A quantum dot may comprise a quantum dot as described in Han et al., “Quantum-dot-tagged microbeads for multiplexed optical coding of biomolecules,” *Nat. Biotechnol.* 19:631-635 (2001); Gao X., “QD barcodes for biosensing and detection,” *Conf Proc IEEE Eng Med Biol Soc* 2009: 6372-6373 (2009); and Zrazhevskiy, et al., “Multicolor multicycle molecular profiling with quantum dots for single-cell analysis,” *Nat Protoc* 8:1852-1869 (2013).

A QD may further comprise a functional group or attachment moiety. One example of such a QD that has a functional group or attachment moiety is a QD with a carboxylic acid terminated surface, such as those commercially available though, for example, Quantum Dot, Inc., Hayward, Calif.

### Conjugating Moiety

The probe may include a conjugating moiety. The conjugation moiety may be attached at the 5' terminus, the 3' terminus, or at an internal site. The conjugating moiety may be a nucleotide analog (such as bromodeoxyuridine). The conjugating moiety may be a conjugating functional group. The conjugating functional group may be an azido group or an alkyne group. The probe may further be derivatized through a chemical reaction such as click chemistry. The click chemistry may be a copper(I)-catalyzed [3+2]-Huisgen 1,3-dipolar cyclo-addition of alkynes and azides leading to 1,2,3-triazoles. The click chemistry may be a copper free variant of the above reaction.

The conjugating moiety may comprise a hapten group. A hapten group may include digoxigenin, 2,4-dinitrophenyl, biotin, avidin, or are selected from azoles, nitroaryl compounds, benzofurazans, triterpenes, ureas, thioureas, rotenones, oxazoles, thiazoles, coumarins, cyclolignans, heterobiaryl compounds, azoaryl compounds or benzodiazepines. A hapten group may include biotin.

The probe comprising the conjugating moiety may further be linked to a second probe (such as a nucleic acid probe or a polypeptide probe), a fluorescent moiety (such as a dye such as a quantum dot), a target nucleic acid, or a conjugating partner such as a polymer (such as PEG), a macromolecule (such as a carbohydrate, a lipid, a polypeptide), and the like.

### Samples

A sample described herein may be a fixed sample. The sample may be subjected to a denaturing condition. The sample may be cryopreserved.

The sample may be a cell sample. The cell sample may be obtained from the cells or tissue of an animal. The animal cell may comprise a cell from an invertebrate, fish, amphibian, reptile, or mammal. The mammalian cell may be obtained from a primate, ape, equine, bovine, porcine, canine, feline, or rodent. The mammal may be a primate, ape, dog, cat, rabbit, ferret, or the like. The rodent may be a mouse, rat, hamster, gerbil, hamster, chinchilla, or guinea pig. The bird cell may be from a canary, parakeet, or parrot. The reptile cell may be from a turtle, lizard, or snake. The fish cell may be from a tropical fish. For example, the fish cell may be from a zebrafish (such as *Danio rerio*). The amphibian cell may be from a frog. An invertebrate cell may be from an insect, arthropod, marine invertebrate, or worm. The worm cell may be from a nematode (such as *Caenorhabditis elegans*). The arthropod cell may be from a tarantula or hermit crab.

The cell sample may be obtained from a mammalian cell. For example, the mammalian cell may be an epithelial cell, connective tissue cell, hormone secreting cell, a nerve cell, a skeletal muscle cell, a blood cell, an immune system cell, or a stem cell. A cell may be a fixed cell, intact cell, or cell lysate.

Cell samples may be cells derived from a cell line. Exemplary cell lines include, but are not limited to, 293A cell line, 293FT cell line, 293F cell line, 293 H cell line, HEK 293 cell line, CHO DG44 cell line, CHO-S cell line, CHO-K1 cell line, Expi293F™ cell line, Flp-In™ T-REX™ 293 cell line, Flp-In™-293 cell line, Flp-In™-3T3 cell line, Flp-In™-BHK cell line, Flp-In™-CHO cell line, Flp-In™-CV-1 cell line, Flp-In™-Jurkat cell line, FreeStyle™ 293-F cell line, FreeStyle™ CHO-S cell line, GripTite™ 293 MSR cell line, GS-CHO cell line, HepaRG™ cell line, T-REX™ Jurkat cell line, Per.C6 cell line, T-REX™-293 cell line, T-REX™-CHO cell line, T-REX™-HeLa cell line, NC-HIMT cell line, and PC12 cell line.

The cell sample may be obtained from cells of a primate. The primate may be a human, or a non-human primate. The cell sample may be obtained from a human. For example, the cell sample may comprise cells obtained from blood, urine, stool, saliva, lymph fluid, cerebrospinal fluid, synovial fluid, cystic fluid, ascites, pleural effusion, amniotic fluid, chorionic villus sample, vaginal fluid, interstitial fluid, buccal swab sample, sputum, bronchial lavage, Pap smear sample, or ocular fluid. The cell sample may comprise cells obtained from a blood sample, an aspirate sample, or a smear sample.

The cell sample may be a circulating tumor cell sample. A circulating tumor cell sample may comprise lymphoma cells, fetal cells, apoptotic cells, epithelia cells, endothelial cells, stem cells, progenitor cells, mesenchymal cells, osteoblast cells, osteocytes, hematopoietic stem cells, foam cells, adipose cells, transcervical cells, circulating cardiocytes, circulating fibrocytes, circulating cancer stem cells, circulating myocytes, circulating cells from a kidney, circulating cells from a gastrointestinal tract, circulating cells from a lung, circulating cells from reproductive organs, circulating cells from a central nervous system, circulating hepatic cells, circulating cells from a spleen, circulating cells from a thymus, circulating cells from a thyroid, circulating cells from an endocrine gland, circulating cells from a parathyroid, circulating cells from a pituitary, circulating cells from an adrenal gland, circulating cells from islets of Langerhans, circulating cells from a pancreas, circulating cells from a hypothalamus, circulating cells from prostate tissues, circulating cells from breast tissues, circulating cells from circulating retinal cells, circulating ophthalmic cells, circulating auditory cells, circulating epidermal cells, circulating cells from the urinary tract, or combinations thereof.

A cell sample may be a peripheral blood mononuclear cell sample.

A cell sample may comprise cancerous cells. The cancerous cells may form a cancer which may be a solid tumor or a hematologic malignancy. The cancerous cell sample may comprise cells obtained from a solid tumor. The solid tumor may include a sarcoma or a carcinoma. Exemplary sarcoma cell sample may include, but are not limited to, cell sample obtained from alveolar rhabdomyosarcoma, alveolar soft part sarcoma, ameloblastoma, angiosarcoma, chondrosarcoma, chordoma, clear cell sarcoma of soft tissue, dedifferentiated liposarcoma, desmoid, desmoplastic small round cell tumor, embryonal rhabdomyosarcoma, epithelioid fibrosarcoma, epithelioid hemangioendothelioma, epithelioid sarcoma, esthesioneuroblastoma, Ewing sarcoma, extrarenal rhabdoid tumor, extraskeletal myxoid chondrosarcoma, extraskeletal osteosarcoma, fibrosarcoma, giant cell tumor, hemangiopericytoma, infantile fibrosarcoma, inflammatory myofibroblastic tumor, Kaposi sarcoma, leiomyosarcoma of bone, liposarcoma, liposarcoma of bone, malignant fibrous histiocytoma (MFH), malignant fibrous histiocytoma (MFH) of bone, malignant mesenchymoma, malignant peripheral nerve sheath tumor, mesenchymal chondrosarcoma, myxofibrosarcoma, myxoid liposarcoma, myxoinflammatory fibroblastic sarcoma, neoplasms with perivascular epithelioid cell differentiation, osteosarcoma, parosteal osteosarcoma, neoplasm with perivascular epithelioid cell differentiation, periosteal osteosarcoma, pleomorphic liposarcoma, pleomorphic rhabdomyosarcoma, PNET/extraskeletal Ewing tumor, rhabdomyosarcoma, round cell liposarcoma, small cell osteosarcoma, solitary fibrous tumor, synovial sarcoma, or telangiectatic osteosarcoma.

Exemplary carcinoma cell samples may include, but are not limited to, cell samples obtained from an anal cancer,

appendix cancer, bile duct cancer (i.e., cholangiocarcinoma), bladder cancer, brain tumor, breast cancer, cervical cancer, colon cancer, cancer of Unknown Primary (CUP), esophageal cancer, eye cancer, fallopian tube cancer, gastroenterological cancer, kidney cancer, liver cancer, lung cancer, medulloblastoma, melanoma, oral cancer, ovarian cancer, pancreatic cancer, parathyroid disease, penile cancer, pituitary tumor, prostate cancer, rectal cancer, skin cancer, stomach cancer, testicular cancer, throat cancer, thyroid cancer, uterine cancer, vaginal cancer, or vulvar cancer.

The cancerous cell sample may comprise cells obtained from a hematologic malignancy. Hematologic malignancy may comprise a leukemia, a lymphoma, a myeloma, a non-Hodgkin's lymphoma, or a Hodgkin's lymphoma. The hematologic malignancy may be a T-cell based hematologic malignancy. The hematologic malignancy may be a B-cell based hematologic malignancy. Exemplary B-cell based hematologic malignancy may include, but are not limited to, chronic lymphocytic leukemia (CLL), small lymphocytic lymphoma (SLL), high risk CLL, a non-CLL/SLL lymphoma, prolymphocytic leukemia (PLL), follicular lymphoma (FL), diffuse large B-cell lymphoma (DLBCL), mantle cell lymphoma (MCL), Waldenström's macroglobulinemia, multiple myeloma, extranodal marginal zone B cell lymphoma, nodal marginal zone B cell lymphoma, Burkitt's lymphoma, non-Burkitt high grade B cell lymphoma, primary mediastinal B-cell lymphoma (PMBL), immunoblastic large cell lymphoma, precursor B-lymphoblastic lymphoma, B cell prolymphocytic leukemia, lymphoplasmacytic lymphoma, splenic marginal zone lymphoma, plasma cell myeloma, plasmacytoma, mediastinal (thymic) large B cell lymphoma, intravascular large B cell lymphoma, primary effusion lymphoma, or lymphomatoid granulomatosis. Exemplary T-cell based hematologic malignancy may include, but are not limited to, peripheral T-cell lymphoma not otherwise specified (PTCL-NOS), anaplastic large cell lymphoma, angioimmunoblastic lymphoma, cutaneous T-cell lymphoma, adult T-cell leukemia/lymphoma (ATLL), blastic NK-cell lymphoma, enteropathy-type T-cell lymphoma, hematosplenic gamma-delta T-cell lymphoma, lymphoblastic lymphoma, nasal NK/T-cell lymphomas, or treatment-related T-cell lymphomas.

A cell sample described herein may comprise a tumor cell line sample. Exemplary tumor cell line sample may include, but are not limited to, cell samples from tumor cell lines such as 600MPE, AU565, BT-20, BT-474, BT-483, BT-549, EvsA-T, Hs578T, MCF-7, MDA-MB-231, SkBr3, T-47D, HeLa, DU145, PC3, LNCaP, A549, H1299, NCI-H460, A2780, SKOV-3/Luc, Neuro2a, RKO, RKO-AS45-1, HT-29, SW1417, SW948, DLD-1, SW480, Capan-1, MC/9, B72.3, B25.2, B6.2, B38.1, DMS 153, SU.86.86, SNU-182, SNU-423, SNU-449, SNU-475, SNU-387, Hs 817.T, LMH, LMH/2A, SNU-398, PLHC-1, HepG2/SF, OCI-Ly1, OCI-Ly2, OCI-Ly3, OCI-Ly4, OCI-Ly6, OCI-Ly7, OCI-Ly10, OCI-Ly18, OCI-Ly19, U2932, DB, HBL-1, RIVA, SUDHL2, TMD8, MEC1, MEC2, 8E5, CCRF-CEM, MOLT-3, TALL-104, AML-193, THP-1, BDCM, HL-60, Jurkat, RPMI 8226, MOLT-4, RS4, K-562, KASUMI-1, Daudi, GA-10, Raji, JeKo-1, NK-92, and Mino.

A cell sample may comprise cells obtained from a biopsy sample, necropsy sample, or autopsy sample.

The cell samples (such as a biopsy sample) may be obtained from an individual by any suitable means of obtaining the sample using well-known and routine clinical methods. Procedures for obtaining tissue samples from an individual are well known. For example, procedures for drawing and processing tissue sample such as from a needle

aspiration biopsy are well-known and may be employed to obtain a sample for use in the methods provided. Typically, for collection of such a tissue sample, a thin hollow needle is inserted into a mass such as a tumor mass for sampling of cells that, after being stained, will be examined under a microscope.

A cell may be a eukaryotic cell. A cell may be a yeast cell. A cell may be a plant cell. A cell may be obtained from an agricultural plant.

#### Detection of a Target Nucleic Acid Sequence

FIG. 26 shows a flowchart for a method 200 of detecting a target nucleic acid sequence. The method may comprise an operation 210 of providing one or more probes capable of binding to a target nucleic acid sequence, as described herein. The method may comprise an operation 220 of binding the one or more probes to the target nucleic acid sequence, as described herein. The method may comprise an operation 230 of detecting a signal associated with binding of the one or more probes to the target nucleic acid sequence, as described herein.

The target nucleic acid sequence may be detected in an intact cell. The target nucleic acid sequence may be detected in a fixed cell. The target nucleic sequence may be detected in a lysate or chromatin spread.

A probe may be used to detect a nucleic acid sequence in a sample. For example, a probe comprising a probe sequence capable of binding a nucleic acid sequence (such as a target nucleic acid sequence) and a detectable label (such as a detectable agent) may be used to detect the nucleic acid sequence. A method for detecting a nucleic acid sequence may comprise contacting a nucleic acid sequence with a probe comprising a probe sequence configured to bind at least a portion of the nucleic acid sequence and detecting the probe (such as detecting the detectable label of the probe). The detection of a nucleic acid sequence may comprise binding the probe to the nucleic acid sequence. For example, the detection of a nucleic acid sequence may comprise binding the probe sequence, such as the sequence of an oligonucleotide probe, to a target nucleic acid sequence. In some cases, the detection of a nucleic acid sequence may comprise hybridizing the probe sequence (such as the nucleic acid binding region) of a nucleic acid probe to a target nucleic acid sequence. The nucleic acid sequence may be a virus nucleic acid sequence. The nucleic acid sequence may be an agricultural viral nucleic acid sequence. The nucleic acid sequence may be a lentivirus nucleic acid sequence, an adenovirus nucleic acid sequence, an adeno-associated virus nucleic acid sequence, or a retrovirus nucleic acid sequence.

A nucleic acid sequence may be contacted with a plurality of probes. A nucleic acid sequence may be contacted with a number of probes ranging from about 1 to about  $10^8$  probes, from about 2 to about  $10^7$  probes, from about 10 to about  $10^6$  probes, from about 100 to about  $10^5$  probes, from about 1,000 to about  $10^4$  probes, from about 1,000 to about 5,000 probes, from about 1,000 probes to about 50,000 probes, from about 1,000 to about  $10^5$  probes, from about 1,000 to about 500,000 probes, from about 1,000 probes to about  $10^6$  probes, from about 1,000 probes to about 50 million probes, or from about 1,000 probes to about  $10^8$  probes. The probes of the plurality of probes may be the same. A plurality of probes may have sequences such that the probes are tiled across the nucleic acid sequence. Each probe can bind to a target nucleic acid sequence along the nucleic acid sequence. The probes of a plurality may be different. A first probe of the plurality of probes may be different than a second probe

of the plurality of probes. The plurality of probes may bind to the nucleic acid sequence with from 0 to 10 nucleotides separating each probe.

A nucleic acid sequence may be washed after it has been contacted with a probe. Washing a nucleic acid sequence after it has been contacted with a probe may reduce background signal for detection of the detectable label of the probe.

A nucleic acid sequence (such as a target nucleic acid sequence) may be contacted by a plurality of probes. A nucleic acid sequence may be contacted with a plurality of types of probes. That is, a method of detection of a nucleic acid sequence (such as a target nucleic acid sequence) may comprise contacting the target nucleic acid sequence with a plurality of sets of probes (such as a plurality of types of probes). A first probe set (such as a first type of probe) may be different from a second probe set (such as a second type of probe) in that the first probe type comprises a first probe sequence which is different than the probe sequence of the second probe type. The probe sequence of a first type of probe may be the same as the probe sequence of a second type of probe. A first probe set may comprise a first detectable label and a first probe sequence and a second probe set may comprise a second detectable label and a second probe sequence, wherein the first and second probe sequences are the same and the first and second detectable labels are different. The first and second probe sequences may be different and the first and second detectable labels of a first and second probe set may be the same. The first and second probe sequences of a first and second probe set may be different and the first and second detectable labels of a first and second probe set may be different. A method of detecting a nucleic acid sequence may comprise contacting a nucleic acid sequence with 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 types of probes.

A first probe sequence may be configured to specifically recognize (such as to bind to or to hybridize with) a first nucleic acid sequence (such as a first target nucleic acid sequence). A second probe sequence may be configured to specifically recognize (such as to bind to or to hybridize with) a second nucleic acid sequence (such as a second target nucleic acid sequence).

A detectable label may be detected with a detector. A detector may detect the signal intensity of the detectable label. A detector may spatially distinguish between two detectable labels. A detector may also distinguish between a first and second detectable label based on the spectral pattern produced by the first and second detectable labels, wherein the first and second detectable label do not produce an identical spectral intensity pattern. For example, a detector may distinguish between a first and second detectable signal, wherein the wavelength of the signal produced by the first detectable label is not the same as the wavelength of the signal produced by the second detectable label. A detector may resolve (such as by spatially distinguishing or spectrally distinguishing) a first and second detectable label that are less than 1 kb apart, less than kb apart, less than kb apart, less than 2 kb apart, less than 2.5 kb apart, less than 3 kb apart, less than 3.5 kb apart, less than 4 kb apart, less than 4.5 kb apart, less than 5 kb apart, less than 5.5 kb apart, less than 6 kb apart, less than 6.5 kb apart, less than 7 kb apart, less than 7.5 kb apart, less than 8 kb apart, less than 8.5 kb apart, less than 9 kb apart, less than 9.5 kb apart, less than 10 kb apart, less than 10.5 kb apart, less than 11 kb apart, less than 11.5 kb apart, less than 12 kb apart, less than 20 kb apart, less than 50 kb apart, or less than 100 kb apart. The detectable label of the probe may be detected optically. For example, a

detectable label of a probe may be detected by light microscopy, fluorescence microscopy, or chromatography. Detection of the detectable label of a probe may comprise stimulating the probe or a portion thereof (such as the detectable label) with a source of radiation (such as a light source, such as a laser). Detection of the detectable label of a probe may also comprise an enzymatic reaction.

Detection of the target nucleic acid sequence may be within a period of not more than 48 hours, not more than 36 hours, not more than 24 hours, not more than 23 hours, not more than 22 hours, not more than 21 hours, not more than 20 hours, not more than 19 hours, not more than 18 hours, not more than 17 hours, not more than 6 hours, not more than 15 hours, not more than 14 hours, not more than 13 hours, or not more than 12 hours.

Determining the presence of a genetic modification in a cell using the Nano-FISH method described herein may be useful is assessing the phenotype of the cell resulting from the genetic modification. A method for assessing a phenotype of an intact genetically modified cell may comprise: a) providing the intact genetically modified cell comprising a target nucleic acid sequence less than 2.5 kilobases in length; b) contacting the intact genetically modified cell with a first plurality of probes, wherein each probe comprises a first detectable label and a probe sequence that binds to a portion of the target nucleic acid sequence; c) detecting a presence of the first detectable label in the intact cell, wherein the presence of the first detectable label indicates the presence of the target nucleic acid sequence; d) determining a phenotype of the intact genetically modified cell; and e) correlating the phenotype of the intact genetically modified cell with the presence of the target nucleic acid sequence. The method may further comprise determining a number or location of genetic modifications in the intact genetically modified cell. The method may further comprise f) selecting a first intact genetically modified cell comprising a phenotype of interest; g) determining a set of conditions used for a genetic modification of the first intact genetically modified cell; and h) preparing a second genetically modified cell using the set of conditions for genetic modification. The intact genetically modified cell may be a eukaryotic cell that was genetically modified. The intact genetically modified cell may be a bacteria cell that was genetically modified. The intact genetically modified cell may be a mammalian cell that was genetically modified. The intact genetically modified cell may be any cell as described herein that was genetically modified. The phenotype may be a product expressed as a result of the genetic modification of the cell. The phenotype may be an increased level or decreased level of the product expressed as a result of the genetic modification of the cell. The phenotype may be an increased quality of the product expressed as a result of the genetic modification of the cell. The expressed product may be protein, such as an enzyme. The expressed product may be a transgene protein, RNA, or a secondary product of the genetic modification. For example, if an enzyme is produced as a result of the genetic modification of the cell, a secondary product of the genetic modification is a product of the enzyme.

Determining the number of target nucleic acid sequences in a cell may be useful in determining the phenotype of the cell. Cells with a specific number of target nucleic acid sequences may be tested for increased cellular activity, decreased cellular activity, or toxicity. Increased cellular activity may be increased expression of a protein or a cellular product. Decreased cellular activity may be decreased expression of a protein or a cellular product.

Toxicity may be a result of cellular activity that may be too high or too low, resulting in cell death. For example, the contacting a sample of cells with a probe configured to bind to a particular target nucleic acid sequence and then determining the number of target nucleic acid sequences in the cell may be an expedient means of determining whether the number of target nucleic acid sequences may be affecting the cell phenotype or function.

A method of detecting or determining the presence of a nucleic acid sequence may comprise determining the number of probes associated with the nucleic acid sequence. A method of detecting or determining the presence of a nucleic acid sequence may comprise determining the number of probes hybridized to the nucleic acid sequence.

It may also be possible to determine the quantity of target nucleic acid sequences in this manner. Quantification of target nucleic acid sequences in a sample using the methods, compositions, and systems described herein may be useful in determining the number of repeated sequences in a nucleic acid of a sample.

Determining the presence, absence, identity, spatial position or sequence position of a target nucleic acid sequence in a sample may be useful in determining a condition of a patient. For example, contacting a patient sample with a probe configured to bind to a particular nucleic acid sequence may be an expedient means of determining whether the patient has the nucleic acid sequence. Similarly, contacting a patient sample with a plurality of types of probes, each configured to bind to a different nucleic acid sequence, may be an expedient means of screening patients for various genetic or acquired conditions, such as inherited mutations.

Determination of the Spatial Position of a Target Nucleic Acid Sequence

FIG. 27 shows a flowchart for a method 300 of determining the spatial position of a nucleic acid sequence. The method may comprise an operation 310 of providing one or more probes capable of binding to a target nucleic acid sequence, as described herein. The method may comprise an operation 320 of binding the one or more probes to the target nucleic acid sequence, as described herein. The method may comprise an operation 330 of imaging a signal associated with binding of the one or more probes to the target nucleic acid sequence, as described herein.

A method of detecting or determining the presence of a nucleic acid sequence may comprise determining the spatial position of a nucleic acid sequence (such as a target nucleic acid sequence). Determining the spatial position of a nucleic acid sequence may comprise contacting a nucleic acid sequence with a probe, which may comprise a detectable label and a probe sequence configured to bind to the nucleic acid sequence, and detecting the detectable label of the probe.

The spatial position of the nucleic acid sequence may be determined relative to features of the sample (such as features of a cell), structures of the sample (such structures or organelles of the cell), or other nucleic acids by using the same or a different imaging modality to detect the reference features, structures, or nucleic acids. For instance, the spatial position of a nucleic acid sequence in a cell relative to the nucleus of a cell by using a plurality of antibodies with a detectable label to counter-label structures of the cell, such as the cell membrane. A cell line expressing a detectable label (such as a fusion protein with a structural protein expressed by the cell) may be used to determine spatial position of a nucleic acid sequence in a cell.

Data collected from detection of all or a portion of the detectable labels in a sample may be used to form one or more two-dimensional images or a three-dimensional rendering or to make calculations determining or estimating the spatial position of the target nucleic acid sequence.

A first probe comprising a first detectable label and a first probe sequence configured to bind to a nucleic acid sequence (such as a target nucleic acid sequence) may be used as a reference position for a second probe comprising a second detectable label and a second probe sequence configured to bind to a second nucleic acid sequence (such as a second target nucleic acid sequence). For example, a first probe specific to a first target nucleic acid sequence of a nucleic acid with a known or anchored position on the nucleic acid may be used as a reference to determine the spatial position of a second target nucleic acid sequence bound by a second probe prior to or during imaging.

Detection of the Sequence Position of a Target Nucleic Acid Sequence

FIG. 28 shows a flowchart for a method 400 of detecting the sequence position of a nucleic acid sequence. The method may comprise an operation 410 of providing a first set of one or more probes capable of binding to one or more reference nucleic acid sequences with known positions in the genome, as described herein. The method may comprise an operation 420 of binding the first set of one or more probes to the one or more reference nucleic acid sequences, as described herein. The method may comprise an operation 430 of providing a second set of one or more probes capable of binding to a target nucleic acid sequence, as described herein. The method may comprise an operation 440 of binding the second set of one or more probes to the target nucleic acid sequence, as described herein. The method may comprise an operation 450 of detecting a signal associated with binding of the first set of one or more probes to the one or more reference nucleic acid sequences and of the second set of one or more probes to the target nucleic acid sequence, as described herein. The method may comprise an operation 460 of comparing the signals associated with binding of the first set of one or more probes to the reference nucleic acid sequences to the signal associated with binding of the second set of one or more probes to the target nucleic acid sequence.

A method of detecting or determining the presence of a nucleic acid sequence may comprise determining the sequence position of a nucleic acid sequence (such as a target nucleic acid sequence). For example, a probe with a probe sequence configured to recognize a first target sequence with a known position in the sequence of a nucleic acid may be used as reference for calculations or estimations of the sequence position of a second target nucleic acid sequence on the nucleic acid. For example, a first probe having a probe sequence configured to recognize a first target sequence with a first known position in the sequence of a nucleic acid and a second probe having a probe sequence configured to recognize a second target nucleic acid sequence with a second known position in the sequence of the nucleic acid may be used as reference points for a third probe configured to recognize a third target nucleic acid sequence with an unknown position in the nucleic acid. The relative sequence position of the third target nucleic acid sequence may be determined or estimated by comparing it to the positions of the first and second target nucleic acid sequences, as indicated by the signals from the first and second probes.

Detection of Target Nucleic Acid Sequences in a Sample Relative to a Control

FIG. 29 shows a flowchart for a method 500 of detecting a nucleic acid in a sample relative to a control. The method may comprise an operation 510 of providing a one or more probes capable of binding to a target nucleic acid sequence in a reference sample and a target nucleic acid sequence in a sample under test, as described herein. The method may comprise an operation 520 of binding the one or more probes to the target nucleic acid sequence in the reference sample and the target nucleic acid sequence in the sample under test, as described herein. The method may comprise an operation 530 of detecting a signal associated with binding of the set of one or more probes to the target nucleic acid sequence in the reference sample and the target nucleic acid sequence in the sample being tested, as described herein. The method may comprise an operation 540 of comparing the signal associated with binding of the one or more probes to the target nucleic acid sequence in the reference sample to the signal associated with binding of the one or more probes to the target nucleic acid sequence in the sample under test, as described herein.

Correlation of the Detection of a Target Nucleic Acid Sequence in a Sample with a Target Protein Expression

The detection of a target nucleic acid sequence in a cell may be correlated with a target protein expression in the same cell. The method may comprise providing a one or more probes capable of binding to a target nucleic acid sequence in a sample and a target nucleic acid sequence in a sample being tested, as described herein, and further comprise providing one or more detectable labels to detect the target protein expression. The presence, absence, or quantity of the detected target nucleic acid sequence may be correlated to the presence, absence, or quantity of the target protein expression. This information may be used to further investigate the relationship between the target nucleic acid sequence and the target protein, and/or how different treatments may perturb this correlation.

Optical Detection of Nucleic Acid Sequences

Described herein is a method of detecting a nucleic acid sequence. The detection may encompass identification of the nucleic acid sequence, determining the presence or absence of the nucleic acid sequence, and/or determining the activity of the nucleic acid sequence. A method of detecting a nucleic acid sequence may include contacting a cell sample with a detection agent, binding the detection agent to the nucleic acid sequence, and analyzing a detection profile from the detection agent to determine the presence, absence, or activity of the nucleic acid sequence.

The method may involve utilizing one or more intrinsic properties associated with a detection agent to aid in detection of the nucleic acid sequence. The intrinsic properties may encompass the size of the detection agent, the intensity of the signal, and the location of the detection agent. The size of the detection agent may include the length of the probe and/or the size of the detectable moiety (such as the size of a fluorescent dye molecule) may modulate the specificity of interaction with a regulatory element. The intensity of the signal from the detection agent may correlate to the sensitivity of detection. For example, a detection agent with a molar extinction coefficient of about  $0.5\text{-}5\times 10^6\text{ M}^{-1}\text{cm}^{-1}$  may have a higher intensity signal relative to a detection agent with a molar extinction coefficient outside of the  $0.5\text{-}5\times 10^6\text{ M}^{-1}\text{cm}^{-1}$  range and may have lower attenuation due to scattering and absorption. Further, a detection agent with a longer excited state lifetime and a large Stoke shift (measured by the distance between the excitation and emis-

sion peaks) may further improve the sensitivity of detection. The location of the detection agent may, for example, provide the activity state of a nucleic acid sequence. A combination of intrinsic properties of the detection agent may be used to detect a regulatory element of interest.

A detection agent may comprise a detectable moiety that is capable of generating a light, and a probe portion that is capable of hybridizing to a target site on a nucleic acid sequence. As described herein, a detection agent may include a DNA probe portion, an RNA probe portion, a polypeptide probe portion, or a combination thereof. A DNA or RNA probe portion may be between about 10 and about 100 nucleotides in length, between about 15 and about 100 nucleotides in length, between about 20 and about 100 nucleotides in length, between about 20 and about 80 nucleotides in length, between about 20 and about 60 nucleotides in length, between about 25 and about 55 nucleotides in length, between about 30 and about 50 nucleotides in length, between about 15 and about 80 nucleotides in length, between about 15 and about 60 nucleotides in length, between about 20 and about 40 nucleotides in length, or between about 20 and about 30 nucleotides in length. A DNA or RNA probe portion may be about 10, about 15, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36, about 37, about 38, about 39, about 40, about 45, about 50, about 55, about 60, about 65, about 70, about 80, about 90, or about 100 nucleotides in length. A DNA or RNA probe portion may be a TALEN probe, ZFN probe, or a CRISPR probe. A DNA or RNA probe portion may be a padlock probe. A polypeptide probe may comprise a DNA-binding protein, a RNA-binding protein, a protein involved in the transcription/translation process or detects the transcription/translation process, a protein that may detect an open or relaxed portion of a chromatin, or a protein interacting partner of a product of a regulatory element (such as an antibody or binding fragment thereof).

In some instances, a detection agent may comprise a DNA or RNA probe portion which may be between about 10 and about 100 nucleotides in length, between about 15 and about 100 nucleotides in length, between about 20 and about 100 nucleotides in length, between about 20 and about 80 nucleotides in length, between about 20 and about 60 nucleotides in length, between about 25 and about 55 nucleotides in length, between about 30 and about 50 nucleotides in length, between about 15 and about 80 nucleotides in length, between about 15 and about 60 nucleotides in length, between about 20 and about 40 nucleotides in length, or between about 20 and about 30 nucleotides in length. A detection agent may comprise a DNA or RNA probe portion which may be about 10, about 15, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36, about 37, about 38, about 39, about 40, about 45, about 50, about 55, about 60, about 65, about 70, about 80, about 90, or about 100 nucleotides in length.

A detection agent may comprise a DNA or RNA probe selected from a TALEN probe, a ZFN probe, or a CRISPR probe.

A set of detection agents may be used to detect a nucleic acid sequence. The set of detection agents may comprise about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 25, about 30, about 35, about 40, about 45, about 50,

or more detection agents. Each of the detection agents within the set of detection agents may recognize and interact with a distinct region of a nucleic acid sequence. About 1, about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, or more detection agents may be used for detection of a nucleic acid sequence. About 1 or more detection agents may be used for detection of a nucleic acid sequence. About 2 or more detection agents may be used for detection of a nucleic acid sequence. About 3 or more detection agents may be used for detection of a nucleic acid sequence. About 4 or more detection agents may be used for detection of a nucleic acid sequence. About 5 or more detection agents may be used for detection of a nucleic acid sequence. About 6 or more detection agents may be used for detection of a nucleic acid sequence. About 7 or more detection agents may be used for detection of a nucleic acid sequence. About 8 or more detection agents may be used for detection of a nucleic acid sequence. About 9 or more detection agents may be used for detection of a nucleic acid sequence. About 10 or more detection agents may be used for detection of a nucleic acid sequence. About 11 or more detection agents may be used for detection of a nucleic acid sequence. About 12 or more detection agents may be used for detection of a nucleic acid sequence. About 13 or more detection agents may be used for detection of a nucleic acid sequence. About 14 or more detection agents may be used for detection of a nucleic acid sequence. About 15 or more detection agents may be used for detection of a nucleic acid sequence. About 20 or more detection agents may be used for detection of a nucleic acid sequence.

A detection agent may comprise a polypeptide probe selected from a DNA-binding protein, a RNA-binding protein, a protein involved in the transcription/translation process or detects the transcription/translation process, a protein that may detect an open or relaxed portion of a chromatin, or a protein interacting partner of a product of a regulatory element (such as an antibody or binding fragment thereof).

A detectable moiety that is capable of generating a light may be directly conjugated or bound to a probe portion. A detectable moiety may indirectly conjugated or bound to a probe portion by a conjugating moiety. As described herein, a detectable moiety may be a small molecule (such as a dye) which may be directly conjugated or bound to a probe portion. A detectable moiety may be a fluorescently labeled protein or molecule which may be attached to a conjugating moiety (such as a hapten group, an azido group, an alkyne group) of a probe.

A profile or a detection profile or signature may include the signal intensity, signal location, and/or size of the signal of the detection agent. The profile or the detection profile may comprise about 100 image frames, about 500 frames, about 1000 frames, about 2000 frames, about 5000 frames, about 10,000 frames, about 20,000 frames, about 30,000 frames, about 40,000 frames, about 50,000 frames, or more image frames. Analysis of the profile or the detection profile may determine the activity of the regulatory element. The degree of activation may also be determined from the analysis of the profile or detection profile. Analysis of the profile or the detection profile may further determine the optical isolation and localization of the detection agents, which may correlate to the localization of the nucleic acid sequence.

FIG. 30 shows a flowchart for a method 600 of fluorescently detecting a target nucleic acid sequence. The method may comprise an operation 610 of providing a one or more

probes capable of binding to a target nucleic acid sequence, as described herein. The method may comprise an operation 620 of binding the one or more probes to the target nucleic acid sequence, as described herein. The method may comprise an operation 630 of photobleaching the one or more probes at one or more wavelengths, as described herein. The method may comprise an operation 640 of detecting a profile of optical emissions associated with the photobleaching, as described herein. The method may comprise an operation 650 of analyzing the detection profile to determine the localization of the target nucleic acid sequence, as described herein.

The localization of a nucleic acid sequence may include contacting a nucleic acid sequence with a first set of detection agents, photobleaching the first set of detection agents for a first time point at a first wavelength to generate a second set of detection agents capable of generating a light at a second wavelength, detecting at least one burst generated by the second set of detection agents to generate a detection profile of the second set of detection agents, and analyzing the detection profile to determine the localization of the nucleic acid sequence.

A detection agent may comprise a detectable moiety that is capable of generating a light, and a probe portion that is capable of hybridizing to a target site on a nucleic acid sequence. Each detection agent within the first set of detection agents may have the same or a different detectable moiety. Each detection agent within the first set of detection agents may have the same detectable moiety. A detectable moiety may comprise a small molecule (such as a fluorescent dye). A detectable moiety may comprise a fluorescently labeled polypeptide, a fluorescently labeled nucleic acid probe, and/or a fluorescently labeled polypeptide complex.

Upon photobleaching, a second set of detection agents may be generated from the first set of detection agents, in which the second set may include detection agents that are capable of generating a burst of light detectable at a second wavelength. For example, bleaching of the set of detection agents may lead to about 50%, about 60%, about 70%, about 80%, about 90%, or more detection agents within the set to enter into an "OFF-state". An "OFF-state" may be a dark state in which the detectable moiety crosses from the singlet excited electronic or ON state to the triplet electronic state or OFF-state in which detection of light (such as fluorescence) may be low (for instance, less than 10%, less than 5%, less than 1%, or less than 0.5% of light may be detected). The remainder of the detection agents that have not entered into the OFF-state may generate bursts of lights, or to cycle between a singlet excited electronic state (or ON-state) and a singlet ground electronic state. As such, bleaching of the set of detection agents may generate about 40%, about 30%, about 20%, about 10%, about 5%, or less detection agents within the set that may generate bursts of lights. The bursts of lights may be detected stochastically, at a single burst level in which each burst of light correlates to a single detection agent.

A single wavelength may be used for photobleaching a set of detection agents. At least two wavelengths may be used for photobleaching a set of detection agents. A wavelength at 491 nm may be used. A wavelength at 405 nm may be used in combination with the wavelength at 491 nm. The two wavelengths may be applied simultaneously to photobleach a set of detection agents. The two wavelengths may be applied sequentially to photobleach a set of detection agents.

The time for photobleaching a set of detection agents may be from about 10 seconds to about 4 hours. The time may be from about 30 seconds to about 3.5 hours, from about one

minute to about 3 hours, from about 5 minutes to about 2 hours, from about 10 minutes to about 1 hour, from about one minutes to about 1 hour, from about 5 minutes to about 1 hour, or from about 30 minutes to about 2 hours. The time may be at least 10 seconds, 20 seconds, 30 seconds, 40 seconds, 50 seconds, 1 minute, 2 minutes, 3 minutes, 4 minutes, 5 minutes, 10 minutes, 15 minutes, 20 minutes, 30 minutes, 45 minutes, 1 hour, 1.5 hours, 2 hours, 2.5 hours, 3 hours, 3.5 hours, 4 hours, or more.

The concentration of the detection agents may be from about 5 nM to about 1  $\mu$ M. The concentration of the detection agent may be from about 5 nM to about 900 nM, from about 10 nM to about 800 nM, from about 15 nM to about 700 nM, from about 20 nM to about 500 nM, from about 10 nM to about 500 nM, from about 10 nM to about 400 nM, from about 10 nM to about 300 nM, from about 10 nM to about 200 nM, from about 10 nM to about 100 nM, from about 50 nM to about 500 nM, from about 50 nM to about 400 nM, from about 50 nM to about 300 nM, from about 50 nM to about 200 nM, from about 100 nM to about 500 nM, from about 100 nM to about 300 nM, or from about 100 nM to about 200 nM. The concentration of the detection agents may be about 10 nM, 15 nM, 20 nM, 30 nM, 40 nM, 50 nM, 60 nM, 70 nM, 80 nM, 90 nM, 100 nM, 150 nM, 200 nM, 250 nM, 300 nM, 400 nM, 500 nM, 600 nM, 700 nM, 800 nM, 900 nM, or more.

The burst of lights from the set of detection agents may generate a detection profile. The detection profile may comprise about 100 image frames, about 500 frames, about 1000 frames, about 2000 frames, about 5000 frames, about 10,000 frames, about 20,000 frames, about 30,000 frames, about 40,000 frames, about 50,000 frames, or more image frames. The detection profile may also include the signal intensity, signal location, or size of the signal. Analysis of the detection profile may determine the optical isolation and localization of the detection agents, which may correlate to the localization of the nucleic acid sequence.

The detection profile may comprise a chromatic aberration correction. The detection profile may comprise less than 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, or 0% chromatic aberration. The detection profile may comprise less than 5% chromatic aberration. The detection profile may comprise less than 4% chromatic aberration. The detection profile may comprise less than 3% chromatic aberration. The detection profile may comprise less than 2% chromatic aberration. The detection profile may comprise less than 1% chromatic aberration. The detection profile may comprise less than 0.5% chromatic aberration. The detection profile may comprise less than 0.1% chromatic aberration. The detection profile may comprise 0% chromatic aberration.

More than one nucleic acid sequence may be detected at the same time. Sometimes, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, or more nucleic acid sequence may be detected at the same time. Each of the nucleic acid sequences may be detected by a set of detection agents. The detectable moiety between the different set of detection agents may be the same. For example, two different sets of detection agents may be used to detect two different nucleic acid sequences and the detectable moieties from the two sets of detection agents may be the same. As such, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, or more nucleic acid sequences may be detected at the same time at the same wavelength. The detectable moiety between the different set of detection agents may also be different. For example, two different sets of detection agents may be used to detect two

different nucleic acid sequences and the detectable moiety from one set of detection agents may be detected at a different wavelength from the detectable moiety of the second set of detection agents. As such, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, or more nucleic acid sequences may be detected at the same time in which each of the nucleic acid sequences may be detected at a different wavelength. The nucleic acid sequence may comprise DNA, RNA, polypeptides, or a combination thereof.

The activity of a target nucleic acid sequence may be measuring utilizing the methods described herein. The methods may include detection of a nucleic acid sequence and one or more products of the nucleic acid sequence. One or more products of the nucleic acid sequence may also include intermediate products or elements. The method may comprise contacting a cell sample with a first set and a second set of detection agents, in which the first set of detection agents interact with a target nucleic acid sequence within the cell and the second set of detection agents interact with at least one product of the target nucleic acid sequence, and analyze a detection profile from the first set and the second set of detection agents, in which the presence or the absence of the at least one product indicates the activity of the target nucleic acid sequence.

As described herein, a detection agent may comprise a detectable moiety that is capable of generating a light, and a probe portion that is capable of hybridizing to a target site on a nucleic acid sequence. Each detection agent within the first set of detection agents may have the same or a different detectable moiety. Each detection agent within the first set of detection agents may have the same detectable moiety. A detectable moiety may comprise a small molecule (such as a fluorescent dye). A detectable moiety may comprise a fluorescently labeled polypeptide, a fluorescently labeled nucleic acid probe, and/or a fluorescently labeled polypeptide complex.

The method may also allow photobleaching of the first set and the second set of detection agents, whereby generating a subset of detection agents capable of generating a burst of light. A detection profile may be generated from the detection of a set of light bursts, in which the presence or the absence of the at least one product may indicate the activity of the target nucleic acid sequence.

The nucleic acid sequence may comprise DNA, RNA, polypeptides, or a combination thereof. The nucleic acid sequence may be DNA. The nucleic acid sequence may be RNA. The nucleic acid sequence may be an enhancer RNA (eRNA). The presence of an eRNA may correlate with target gene transcription that is downstream of eRNA. The nucleic acid sequence may be a DNaseI hypersensitive site (DHS). The DHS may be an activated DHS. The pattern of the DHS on a chromatin may correlate to the activity of the chromatin. The nucleic acid sequence may be a polypeptide, such as a transcription factor, a DNA or RNA-binding protein or binding fragment thereof, or a polypeptide that is involved in chemical modification. The nucleic acid sequence may be chromatin.

#### Epifluorescence Imaging

One or more far-field or near-field fluorescence techniques may be utilized for the detection, localization, activity determination, and mapping of one or more nucleic acid sequences described herein. A microscopy method may be a high magnification oil immersion microscopy method. In such a method, wide-field and/or confocal fluorescent microscopes may achieve sub-cellular resolution.

#### Super-Resolution Imaging

A microscopy method may utilize a super-resolution microscopy, which allows images to be taken with a higher resolution than the diffraction limit. A super-resolution microscopy method may utilize a deterministic super-resolution microscopy method, which utilizes a fluorophore's nonlinear response to excitation to enhance resolution. Exemplary deterministic super-resolution methods may include stimulated emission depletion (STED), ground state depletion (GSD), reversible saturable optical linear fluorescence transitions (RESOLFT), and/or saturated structured illumination microscopy (SSIM). A super-resolution microscopy method may also include a stochastic super-resolution microscopy method, which utilizes a complex temporal behavior of a fluorophore, to enhance resolution. Exemplary stochastic super-resolution method may include super-resolution optical fluctuation imaging (SOFI), all single-molecular localization method (SMLM) such as spectral precision determination microscopy (SPDM), SPDMphymod, photo-activated localization microscopy (PALM), fluorescence photo-activated localization microscopy (FPALM), stochastic optical reconstruction microscopy (STORM), and dSTROM.

A microscopy method may be a single-molecular localization method (SMLM). A microscopy method may be a spectral precision determination microscopy (SPDM) method. A SPDM method may rely on stochastic burst or blinking of fluorophores and subsequent temporal integration of signals to achieve lateral resolution at, for example, between about 10 nm and about 100 nm.

A microscopy method may be a spatially modulated illumination (SMI) method. A SMI method may utilize phased lasers and interference patterns to illuminate specimens and increase resolution by measuring the signal in fringes of the resulting Moire patterns.

A microscopy method may be a synthetic aperture optics (SAO) method. A SAO method may utilize a low magnification, low numerical aperture (NA) lens to achieve large field of view and depth of field, without sacrificing spatial resolution. For example, an SAO method may comprise illuminating the detection agent-labeled target (such as a target nucleic acid sequence) with a predetermined number (N) of selective excitation patterns, where the number (N) of selective excitation patterns is determined based upon the detection agent's physical characteristics corresponding to spatial frequency content (such as the size, shape, and/or spacing of the detection agents on the imaging target) from the illuminated target, optically imaging the illuminated target at a resolution insufficient to resolve the objects on the target, and processing optical images of the illuminated target using information on the selective excitation patterns to obtain a final image of the illuminated target at a resolution sufficient to resolve the objects on the target. The number (N) of selective excitation patterns may correspond to the number of k-space sampling points in a k-space sampling space in a frequency domain, with the extent of the k-space sampling space being substantially proportional to an inverse of a minimum distance (4x) between the objects that is to be resolved by SAO, and with the inverse of the k-space sampling interval between the k-space sampling points being less than a width (w) of a detected area captured by a pixel of a system for said optical imaging. The number (N) may include a function of various parameters of the imaging system (such as a magnification of the objective lens, numerical aperture of the objective lens, wavelength of

the light emitted from the imaging target, and/or effective pixel size of the pixel sensitive area of the image detector, etc.).

A SAO method may analyze a set of detection agent profiles from at least 100, at least 200, at least 250, at least 500, at least 1000, or more cells imaged simultaneously within one field of view utilizing an imaging instrument. The one field of view may be a single wide field of view allowing image capture of at least 100, at least 200, at least 250, at least 500, at least 1000, or more cells. The single wide field of view may be about 0.70 mm by about 0.70 mm field of view. The SAO imaging instrument may enable a resolution of about 0.25  $\mu\text{m}$  with a 20 $\times$ /0.45NA lens. The SAO imaging instrument may enable a depth of field of about 2.72  $\mu\text{m}$  with a 20 $\times$ /0.45NA lens. The imaging instrument may enable a working distance of about 7 mm with a 20 $\times$ /0.45NA lens. The imaging instrument may enable a z-stack of 1 with a 20 $\times$ /0.45NA lens. The SAO method may further integrate and interpolate 3-dimensional images from 2-dimensional images.

The SAO imaging instrument may be an SAO instrument as described in U.S. Publication No. 2011/0228073 (Light-speed Genomics, Inc).

#### Analysis of Fluorescence Images

FIG. 31 shows a flowchart for a method 700 of analyzing a fluorescence image of one or more target nucleic acid sequences. The method may comprise an operation 710 of obtaining a fluorescence image of one or more probes bound to one or more target nucleic acid sequences, as described herein. The method may comprise an operation 720 of deconvolving the image one or more times, as described herein. The method may comprise an operation 730 of generating a two-dimensional region of interest (ROI) mask from the deconvolved image, as described herein. The method may comprise an operation 740 of generating a three-dimensional ROI mask from the two-dimensional ROI mask, as described herein. The method may comprise an operation 750 of refining the three-dimensional ROI mask, as described herein. The method may comprise an operation 760 of analyzing the three-dimensional ROI mask to determine the locations of all target nucleic acid sequences, as described herein.

Images obtained using the systems and methods described herein may be subjected to an image analysis method. The images may be obtained using the epifluorescence imaging systems and methods described herein. The image may be obtained using the super-resolution imaging systems and methods described herein. The image analysis method may allow a quantitative morphometric analysis to be conducted on regions of interest (ROIs) within the images.

The image analysis method may comprise a deconvolution of the image. The image analysis method may comprise an iterative deconvolution of the image. The image analysis method may comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 iterations of deconvolving the image. The image analysis method may comprise more than 1, more than 2, more than 3, more than 4, more than 5, more than 6, more than 7, more than 8, more than 9, or more than 10 iterations of deconvolving the image. The deconvolution procedure may reduce out-of-focus blur in the epifluorescence images or super-resolution images, enhancing the signal-to-noise ratio (SNR) within ROIs.

The image analysis method may further comprise an identification of the ROIs. The ROIs may be identified using an automated detection method.

The image analysis method may further comprise segmentation of the ROIs. This may allow the rapid delineation of ROIs within the epifluorescence or super-resolution

images. The segmentation of ROIs may comprise utilizing a maximum intensity projection image to generate a two-dimensional ROI mask. The two-dimensional ROI mask may act as a template for an initial three-dimensional mask. For instance, the initial three-dimensional mask may be generated by projecting the two-dimensional ROI mask into a third spatial dimension. The projection may be a weighted projection. The initial three-dimensional mask may be further refined to obtain a refined three-dimensional ROI mask. Refinement of the initial three-dimensional mask may be achieved utilizing adaptive thresholding and/or region growing methods. Refinement of the initial three-dimensional mask may be achieved by iteratively applying adaptive thresholding and/or region growing methods. The iterative procedure may result in a final three-dimensional ROI mask. The final three-dimensional ROI mask may comprise information regarding the locations of all FISH-labeled nucleic acid sequences within each cell in a sample.

The image analysis method may be implemented in an automated manner, such as using the digital processing devices described herein.

#### Digital Processing Device

The systems, apparatus, and methods described herein may include a digital processing device, or use of the same. The digital processing device may include one or more hardware central processing units (CPU) that carry out the device's functions. The digital processing device may further comprise an operating system configured to perform executable instructions. In some instances, the digital processing device is optionally connected to a computer network, is optionally connected to the Internet such that it accesses the World Wide Web, or is optionally connected to a cloud computing infrastructure. In other instances, the digital processing device is optionally connected to an intranet. In other instances, the digital processing device is optionally connected to a data storage device.

In accordance with the description herein, suitable digital processing devices may include, by way of non-limiting examples, server computers, desktop computers, laptop computers, notebook computers, sub-notebook computers, netbook computers, netpad computers, set-top computers, media streaming devices, handheld computers, Internet appliances, mobile smartphones, tablet computers, personal digital assistants, video game consoles, and vehicles. Those of skill in the art will recognize that many smartphones are suitable for use in the system described herein. Those of skill in the art will also recognize that select televisions, video players, and digital music players with optional computer network connectivity are suitable for use in the system described herein. Suitable tablet computers may include those with booklet, slate, and convertible configurations, known to those of skill in the art.

The digital processing device may include an operating system configured to perform executable instructions. The operating system may be, for example, software, including programs and data, which may manage the device's hardware and provides services for execution of applications. Those of skill in the art will recognize that suitable server operating systems may include, by way of non-limiting examples, FreeBSD, OpenBSD, NetBSD®, Linux, Apple® Mac OS X Server®, Oracle® Solaris®, Windows Server®, and Novell® NetWare®. Those of skill in the art will recognize that suitable personal computer operating systems include, by way of non-limiting examples, Microsoft® Windows®, Apple® Mac OS X®, UNIX®, and UNIX-like operating systems such as GNU/Linux®. In some cases, the operating system is provided by cloud computing. Those of

skill in the art will also recognize that suitable mobile smart phone operating systems include, by way of non-limiting examples, Nokia® Symbian® OS, Apple® iOS®, Research In Motion® BlackBerry OS®, Google® Android®, Microsoft® Windows Phone® OS, Microsoft® Windows Mobile® OS, Linux®, and Palm® WebOS®. Those of skill in the art will also recognize that suitable media streaming device operating systems include, by way of non-limiting examples, Apple TV®, Roku®, Boxee®, GoogleTV®, GoogleChromecast®, AmazonFire®, and Samsung® HomeSync®. Those of skill in the art will also recognize that suitable video game console operating systems include, by way of non-limiting examples, Sony® PS3®, Sony® PS4®, Microsoft® Xbox 360®, Microsoft Xbox One, Nintendo® Wii®, Nintendo® Wii U®, and Ouya®.

In some instances, the device may include a storage and/or memory device. The storage and/or memory device may be one or more physical apparatuses used to store data or programs on a temporary or permanent basis. In some instances, the device is volatile memory and requires power to maintain stored information. In other instances, the device is non-volatile memory and retains stored information when the digital processing device is not powered. In still other instances, the non-volatile memory comprises flash memory. The non-volatile memory may comprise dynamic random-access memory (DRAM). The non-volatile memory may comprise ferroelectric random access memory (FRAM). The non-volatile memory may comprise phase-change random access memory (PRAM). The device may be a storage device including, by way of non-limiting examples, CD-ROMs, DVDs, flash memory devices, magnetic disk drives, magnetic tapes drives, optical disk drives, and cloud computing based storage. The storage and/or memory device may also be a combination of devices such as those disclosed herein.

The digital processing device may include a display to send visual information to a user. The display may be a cathode ray tube (CRT). The display may be a liquid crystal display (LCD). Alternatively, the display may be a thin film transistor liquid crystal display (TFT-LCD). The display may further be an organic light emitting diode (OLED) display. In various cases, on OLED display is a passive-matrix OLED (PMOLED) or active-matrix OLED (AMOLED) display. The display may be a plasma display. The display may be a video projector. The display may be a combination of devices such as those disclosed herein.

The digital processing device may also include an input device to receive information from a user. For example, the input device may be a keyboard. The input device may be a pointing device including, by way of non-limiting examples, a mouse, trackball, track pad, joystick, game controller, or stylus. The input device may be a touch screen or a multi-touch screen. The input device may be a microphone to capture voice or other sound input. The input device may be a video camera or other sensor to capture motion or visual input. Alternatively, the input device may be a Kinect™, Leap Motion™, or the like. In further aspects, the input device may be a combination of devices such as those disclosed herein.

#### Non-Transitory Computer Readable Storage Medium

In some instances, the systems, apparatus, and methods disclosed herein may include one or more non-transitory computer readable storage media encoded with a program including instructions executable by the operating system of an optionally networked digital processing device. In further instances, a computer readable storage medium is a tangible component of a digital processing device. In still further

instances, a computer readable storage medium is optionally removable from a digital processing device. A computer readable storage medium may include, by way of non-limiting examples, CD-ROMs, DVDs, flash memory devices, solid state memory, magnetic disk drives, magnetic tape drives, optical disk drives, cloud computing systems and services, and the like. In some cases, the program and instructions are permanently, substantially permanently, semi-permanently, or non-transitorily encoded on the media. Computer Program

The systems, apparatus, and methods disclosed herein may include at least one computer program, or use of the same. A computer program includes a sequence of instructions, executable in the digital processing device's CPU, written to perform a specified task. In some embodiments, computer readable instructions are implemented as program modules, such as functions, objects, Application Programming Interfaces (APIs), data structures, and the like, that perform particular tasks or implement particular abstract data types. In light of the disclosure provided herein, those of skill in the art will recognize that a computer program, in certain embodiments, is written in various versions of various languages.

The functionality of the computer readable instructions may be combined or distributed as desired in various environments. A computer program may comprise one sequence of instructions. A computer program may comprise a plurality of sequences of instructions. In some instances, a computer program is provided from one location. In other instances, a computer program is provided from a plurality of locations. In additional cases, a computer program includes one or more software modules. Sometimes, a computer program may include, in part or in whole, one or more web applications, one or more mobile applications, one or more standalone applications, one or more web browser plug-ins, extensions, add-ins, or add-ons, or combinations thereof.

#### Web Application

A computer program may include a web application. In light of the disclosure provided herein, those of skill in the art will recognize that a web application, in various aspects, utilizes one or more software frameworks and one or more database systems. In some cases, a web application is created upon a software framework such as Microsoft® .NET or Ruby on Rails (RoR). In some cases, a web application utilizes one or more database systems including, by way of non-limiting examples, relational, non-relational, object oriented, associative, and XML database systems. Sometimes, suitable relational database systems may include, by way of non-limiting examples, Microsoft® SQL Server, MySQL™ and Oracle®. Those of skill in the art will also recognize that a web application, in various instances, is written in one or more versions of one or more languages. A web application may be written in one or more markup languages, presentation definition languages, client-side scripting languages, server-side coding languages, database query languages, or combinations thereof. A web application may be written to some extent in a markup language such as Hypertext Markup Language (HTML), Extensible Hypertext Markup Language (XHTML), or eXtensible Markup Language (XML). In some embodiments, a web application is written to some extent in a presentation definition language such as Cascading Style Sheets (CSS). A web application may be written to some extent in a client-side scripting language such as Asynchronous Javascript and XML (AJAX), Flash® Actionscript, Javascript, or Silverlight®. A web application may be written to some extent in

a server-side coding language such as Active Server Pages (ASP), ColdFusion®, Perl, Java™, JavaServer Pages (JSP), Hypertext Preprocessor (PHP), Python™, Ruby, Tcl, Smalltalk, WebDNA®, or Groovy. Sometimes, a web application may be written to some extent in a database query language such as Structured Query Language (SQL). Other times, a web application may integrate enterprise server products such as IBM® Lotus Domino®. In some instances, a web application includes a media player element. In various further instances, a media player element utilizes one or more of many suitable multimedia technologies including, by way of non-limiting examples, Adobe® Flash®, HTML 5, Apple® QuickTime®, Microsoft® Silverlight®, Java™, and Unity®.

#### Mobile Application

A computer program may include a mobile application provided to a mobile digital processing device. In some cases, the mobile application is provided to a mobile digital processing device at the time it is manufactured. In other cases, the mobile application is provided to a mobile digital processing device via the computer network described herein.

In view of the disclosure provided herein, a mobile application is created by techniques known to those of skill in the art using hardware, languages, and development environments known to the art. Those of skill in the art will recognize that mobile applications are written in several languages. Suitable programming languages include, by way of non-limiting examples, C, C++, C #, Objective-C, Java™, Javascript, Pascal, Object Pascal, Python™, Ruby, VB.NET, WML, and XHTML/HTML with or without CSS, or combinations thereof.

Suitable mobile application development environments are available from several sources. Commercially available development environments include, by way of non-limiting examples, AirplaySDK, alcheMo, Appcelerator®, Celsius, Bedrock, Flash Lite, .NET Compact Framework, Rhomobile, and WorkLight Mobile Platform. Other development environments are available without cost including, by way of non-limiting examples, Lazarus, MobiFlex, MoSync, and Phoneygap. Also, mobile device manufacturers distribute software developer kits including, by way of non-limiting examples, iPhone and iPad (iOS) SDK, Android™ SDK, BlackBerry® SDK, BREW SDK, Palm® OS SDK, Symbian SDK, webOS SDK, and Windows® Mobile SDK.

Those of skill in the art will recognize that several commercial forums are available for distribution of mobile applications including, by way of non-limiting examples, Apple® App Store, Android™ Market, BlackBerry® App World, App Store for Palm devices, App Catalog for webOS, Windows® Marketplace for Mobile, Ovi Store for Nokia® devices, Samsung® Apps, and Nintendo® DSi Shop.

#### Standalone Application

A computer program may include a standalone application, which is a program that is run as an independent computer process, not an add-on to an existing process, e.g., not a plug-in. Those of skill in the art will recognize that standalone applications are often compiled. A compiler is a computer program(s) that transforms source code written in a programming language into binary object code such as assembly language or machine code. Suitable compiled programming languages include, by way of non-limiting examples, C, C++, Objective-C, COBOL, Delphi, Eiffel, Java™, Lisp, Python™, Visual Basic, and VB .NET, or combinations thereof. Compilation is often performed, at

least in part, to create an executable program. A computer program may include one or more executable compiled applications.

#### Web Browser Plug-in

The computer program may include a web browser plug-in. In computing, a plug-in is one or more software components that add specific functionality to a larger software application. Makers of software applications support plug-ins to enable third-party developers to create abilities which extend an application, to support easily adding new features, and to reduce the size of an application. When supported, plug-ins enable customizing the functionality of a software application. For example, plug-ins are commonly used in web browsers to play video, generate interactivity, scan for viruses, and display particular file types. Those of skill in the art will be familiar with several web browser plug-ins including, Adobe® Flash® Player, Microsoft® Silverlight®, and Apple® QuickTime®. In some embodiments, the toolbar comprises one or more web browser extensions, add-ins, or add-ons. In some embodiments, the toolbar comprises one or more explorer bars, tool bands, or desk bands.

In view of the disclosure provided herein, those of skill in the art will recognize that several plug-in frameworks are available that enable development of plug-ins in various programming languages, including, by way of non-limiting examples, C++, Delphi, Java™ PHP, Python™, and VB .NET, or combinations thereof.

Web browsers (also called Internet browsers) may be software applications, designed for use with network-connected digital processing devices, for retrieving, presenting, and traversing information resources on the World Wide Web. Suitable web browsers include, by way of non-limiting examples, Microsoft® Internet Explorer®, Mozilla® Firefox®, Google® Chrome, Apple® Safari®, Opera Software® Opera®, and KDE Konqueror. In some embodiments, the web browser is a mobile web browser. Mobile web browsers (also called microbrowsers, mini-browsers, and wireless browsers) are designed for use on mobile digital processing devices including, by way of non-limiting examples, handheld computers, tablet computers, netbook computers, subnotebook computers, smartphones, music players, personal digital assistants (PDAs), and handheld video game systems. Suitable mobile web browsers include, by way of non-limiting examples, Google® Android® browser, RIM BlackBerry® Browser, Apple® Safari®, Palm® Blazer, Palm® WebOS® Browser, Mozilla® Firefox® for mobile, Microsoft® Internet Explorer® Mobile, Amazon® Kindle® Basic Web, Nokia® Browser, Opera Software® Opera® Mobile, and Sony® PSP™ browser.

#### Software Modules

The systems and methods disclosed herein may include software, server, and/or database modules, or use of the same. In view of the disclosure provided herein, software modules may be created by techniques known to those of skill in the art using machines, software, and languages known to the art. The software modules disclosed herein may be implemented in a multitude of ways. A software module may comprise a file, a section of code, a programming object, a programming structure, or combinations thereof. A software module may comprise a plurality of files, a plurality of sections of code, a plurality of programming objects, a plurality of programming structures, or combinations thereof. In various aspects, the one or more software modules comprise, by way of non-limiting examples, a web application, a mobile application, and a standalone application. In some instances, software modules are in one com-

puter program or application. In other instances, software modules are in more than one computer program or application. In some cases, software modules are hosted on one machine. In other cases, software modules are hosted on more than one machine. Sometimes, software modules may be hosted on cloud computing platforms. Other times, software modules may be hosted on one or more machines in one location. In additional cases, software modules are hosted on one or more machines in more than one location. Databases

The methods, apparatus, and systems disclosed herein may include one or more databases, or use of the same. In view of the disclosure provided herein, those of skill in the art will recognize that many databases are suitable for storage and retrieval of analytical information described elsewhere herein. In various aspects described herein, suitable databases may include, by way of non-limiting examples, relational databases, non-relational databases, object oriented databases, object databases, entity-relationship model databases, associative databases, and XML databases. A database may be internet-based. A database may be web-based. A database may be cloud computing-based. Alternatively, a database may be based on one or more local computer storage devices.

#### Services

Methods and systems described herein may further be performed as a service. For example, a service provider may obtain a sample that a customer wishes to analyze. The service provider may then encode the sample to be analyzed by any of the methods described herein, performs the analysis and provides a report to the customer. The customer may also perform the analysis and provides the results to the service provider for decoding. In some instances, the service provider then provides the decoded results to the customer. In other instances, the customer may receive encoded analysis of the samples from the provider and decodes the results by interacting with softwares installed locally (at the customer's location) or remotely (e.g., on a server reachable through a network). Sometimes, the softwares may generate a report and transmit the report to the customer. Exemplary customers include clinical laboratories, hospitals, industrial manufacturers and the like. Sometimes, a customer or party may be any suitable customer or party with a need or desire to use the methods provided herein.

#### Server

The methods provided herein may be processed on a server or a computer server, as shown in FIG. 32). The server 801 may include a central processing unit (CPU, also "processor") 805 which may be a single core processor, a multi core processor, or plurality of processors for parallel processing. A processor used as part of a control assembly may be a microprocessor. The server 801 may also include memory 810 (e.g., random access memory, read-only memory, flash memory); electronic storage unit 815 (e.g., hard disk); communications interface 820 (e.g., network adaptor) for communicating with one or more other systems; and peripheral devices 825 which includes cache, other memory, data storage, and/or electronic display adaptors. The memory 810, storage unit 815, interface 820, and peripheral devices 825 may be in communication with the processor 805 through a communications bus (solid lines), such as a motherboard. The storage unit 815 may be a data storage unit for storing data. The server 801 may be operatively coupled to a computer network ("network") 830 with the aid of the communications interface 820. A processor with the aid of additional hardware may also be operatively coupled to a network. The network 830 may be the Internet,

an intranet and/or an extranet, an intranet and/or extranet that is in communication with the Internet, a telecommunication or data network. The network 830 with the aid of the server 801, may implement a peer-to-peer network, which may enable devices coupled to the server 801 to behave as a client or a server. The server may be capable of transmitting and receiving computer-readable instructions (e.g., device/system operation protocols or parameters) or data (e.g., sensor measurements, raw data obtained from detecting metabolites, analysis of raw data obtained from detecting metabolites, interpretation of raw data obtained from detecting metabolites, etc.) via electronic signals transported through the network 830. Moreover, a network may be used, for example, to transmit or receive data across an international border.

The server 801 may be in communication with one or more output devices 835 such as a display or printer, and/or with one or more input devices 840 such as, for example, a keyboard, mouse, or joystick. The display may be a touch screen display, in which case it functions as both a display device and an input device. Different and/or additional input devices may be present such an enunciator, a speaker, or a microphone. The server may use any one of a variety of operating systems, such as for example, any one of several versions of Windows®, or of MacOS®, or of Unix®, or of Linux®.

The storage unit 815 may store files or data associated with the operation of a device, systems or methods described herein.

The server may communicate with one or more remote computer systems through the network 830. The one or more remote computer systems may include, for example, personal computers, laptops, tablets, telephones, Smart phones, or personal digital assistants.

A control assembly may include a single server 801. In other situations, the system may include multiple servers in communication with one another through an intranet, extranet and/or the Internet.

The server 801 may be adapted to store device operation parameters, protocols, methods described herein, and other information of potential relevance. Such information may be stored on the storage unit 815 or the server 801 and such data is transmitted through a network.

#### Kits

A composition described herein may be supplied in the form of a kit. A composition may be a probe set designed for a target nucleic acid sequence. The kits of the present disclosure may further comprise instructions regarding the method of using the probe set to detect the target nucleic acid sequence.

In some embodiments, a kit comprises the compositions and methods for detecting a target nucleic acid sequence (to perform a Nano-FISH assay). The compositions and methods may be for fast detection of the target nucleic acid sequence, e.g., in about 24 hours or less, or in about 48 hours or less. The compositions and methods may be for detection of the target nucleic acid sequence, wherein the target nucleic acid sequence is a short nucleic acid sequence, e.g., less than 2 kb, less than 1.5 kb, or less than 0.5 kb. The compositions and methods may be for detecting and quantifying the target nucleic acid sequence in a cell or in a population of cells. In some embodiments, a kit may further comprise components useful in using the kit components and instructions on how to prepare the components for detection of a target nucleic acid sequence. In some embodiments, the kit may further comprise software needed for detection of the target nucleic acid sequence.

The components of the kit may be in dry or liquid form. If they are in dry form, the kit may include a solution to solubilize the dried material. The kit may also include transfer factor in liquid or dry form. In some embodiments, if the transfer factor is in dry form, the kit includes a solution to solubilize the transfer factor. The kit may also include containers for mixing and preparing the components. The kits as described herein also may include a means for containing compositions of the present disclosure in close confinement for commercial sale and distribution.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of skill in the art to which the claimed subject matter belongs. It is to be understood that the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of any subject matter claimed. In this application, the use of the singular includes the plural unless specifically stated otherwise. It must be noted that, as used in the specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the context clearly dictates otherwise. In this application, the use of "or" means "and/or" unless stated otherwise. Furthermore, use of the term "including" as well as other forms, such as "include", "includes," and "included," is not limiting.

As used herein, ranges and amounts may be expressed as "about" a particular value or range. About also includes the exact amount. Hence "about 5  $\mu$ L" means "about 5  $\mu$ L" and also "5  $\mu$ L." Generally, the term "about" includes an amount that would be expected to be within experimental error.

The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

## EXAMPLES

These examples are provided for illustrative purposes only and not to limit the scope of the claims provided herein.

### Example 1

#### DNase Treatment and TUNEL Assay

A TUNEL assay as described below may be used to label DNaseI cut sites on a global cell. For example, all of the DNaseI cut sites within a cell's nucleus may be labeled.

Cells were prepared for a 2-color SPDM for DNA density and DNase I sensitivity (TUNEL) assay.

An adherent cell line, A549 (lung adenocarcinoma), was used for these experiments. They were plated overnight on uncoated 18 mm (#1 thickness) coverslips. Cells were deliberately plated sparsely to be ~20% confluent on the day of the assay.

For all coverslips, cells were fixed with 4% formaldehyde in PBS for 10 minutes at room temperature, and then equilibrated in buffer A at room temperature for 15 minutes. The cells were permeabilized with 0.1% NP-40 in buffer A for 10 minutes at room temperature.

The DNaseI assay was performed with 80 U/ml DNaseI for 3 minutes at 37° C. Cells were then post fixed in 4% formaldehyde in buffer A for 10 minutes at room temperature. The coverslips were permeabilized for 20 minutes with buffer A with 0.25% TX-100, and washed twice with distilled water and were equilibrated with 100  $\mu$ l of TdT terminal deoxynucleotide transferase (TdT) reaction with

EdUTP-alkyne (100  $\mu$ l per coverslip) was performed for 1 hour at 37° C. At the end of the TdT reaction, the coverslips were washed twice with 3% BSA/PBS. The ClickIT reaction was then performed for 2 coverslips to add Alexafluor647 to incorporated EdUTP-alkyne. This reaction was performed for 30 minutes at room temperature, in the dark. The other coverslips were kept in 3% BSA/PBS at room temperature. The coverslips were washed once with 3% BSA/PBS before being stained with Vybrant Violet staining and imaged by a SMLM method.

FIG. 3A shows a two color SPDM image (experimental) of chromatin (blue) with a DNA sensitive element (red), showing anti-colocalization of the DNA sensitive element with chromatin. Scale bars: 1000 nm, inserts: 100 nm. FIG. 3B is the inset of FIG. 3A.

FIG. 4A and FIG. 4B illustrate the localization precision and nearest neighbor distances for DNA and DNase sensitive elements.

### Example 2

#### DNA Encoding of Molecular Targets on a Multi-Omics Imaging Platform

Integration of imaging data across different molecular target types may provide in-depth insights into cell physiology and pathology. A multi-omics imaging platform is utilized which enables simultaneous visualization of multiple molecular targets irrespective of target type and imaging probes used. The multi-omics imaging platform comprises (i) decoupling of target binding and labeling steps, (ii) translation of heterogeneous molecular information into an intermediate standardized molecular code amenable to read-out via imaging probes, and (iii) employing encoding capacity and self-assembly capabilities of DNA bonding. Specifically, molecular targets of interest are first encoded with unique ssDNA tags via binding by ssDNA-conjugated target-recognition moieties under optimized conditions favoring specific target binding. Individual ssDNA tags are then converted into detectable signals via sequence-specific hybridization with complementary ssDNA'-conjugated imaging probes under probe-optimized conditions. As such, molecular target uniqueness, localization, abundance, and specimen morphology information are preserved through all steps of labeling procedure, producing comprehensive molecular signatures of a physiological or pathological process.

#### Methods

##### Oligonucleotide Probe Design.

Sequences for 6 ssDNA/ssDNA' encoding pairs were selected from a random pool. Selection criteria were: continuous 16 bp complementarity, balanced nucleotide composition, lack of stable secondary structures at room temperature, lack of substantial cross-hybridization between mismatch pairs. See TABLE 4 for a complete list of ssDNA/ssDNA' encoding pairs.

Sequences for human GAPDH mRNA (NM\_002046.5) and HSP90-alpha mRNA (NM\_001271969.1) were obtained from NCBI. Sets of mRNA in situ hybridization (ISH) probes were designed using Stellaris RNA FISH Probe Designer (Biosearch Technologies). Probe sets contained 36 unique probes for GAPDH mRNA and 48 probes for HSP90-alpha mRNA. Each probe featured 5' terminal 20nt-long region complementary to mRNA, a spacer (either AAAAA for smaller 41nt probes or AAAAA-dsSpacer-AAAA for longer 60nt probes), and a 16nt-long QDot binding tag. The ISH probe strand of the dsSpacer was

5'-TTCCCAAGCGTCATCT-3' (SEQ ID NO: 941), pre-hybridized with a complementary 5'-AGATGACGCTTGG-GAA-3' ssDNA (SEQ ID NO: 1032) at a 1:1 molar ratio to form a 16 bp dsDNA spacer prior to specimen labeling. See TABLE 5 and TABLE 6 for a complete list of ISH probes. All oligonucleotides were purchased from IDT DNA.

#### Antibody-ssDNA Conjugation.

Purified primary and secondary antibodies in PBS were purchased from Sigma-Aldrich. Amine-terminated HPLC purified ssDNA tags were purchased from IDT DNA (see TABLE 4, Tag IDs 1B-6B). Covalent antibody-ssDNA bioconjugation was achieved either a) via maleimide-mediated amine-sulfhydryl crosslinking or b) using Thunder-Link oligo conjugation system (Innova Biosciences).

For maleimide-mediated crosslinking, IgG was partially reduced by TCEP to expose free sulfhydryl groups, while 5' amine-terminated ssDNA oligonucleotides were activated by sulfo-SMCC (Thermo Scientific). IgG was diluted to 1 mg/mL in 100  $\mu$ L PBS with 10 mM EDTA, mixed with 0.5 mM TCEP, and incubated for 30 min at 37° C. At the same time, ssDNA was diluted to 40  $\mu$ M in 100  $\mu$ L PBS, mixed with 10 mM sulfo-SMCC, and incubated for 30 min at RT. Reduced IgG and activated ssDNA were then purified by 3 rounds of desalting in Zeba desalting spin columns (Thermo Scientific) pre-washed with PBS/10 mM EDTA, mixed, and reacted for 4 hrs at room temperature (RT). Finally, unreacted sulfhydryl groups were capped by addition of 1 mM sulfo-SMCC pre-quenched by excess glycine. Antibody-ssDNA bioconjugates were purified by ultrafiltration for at least 6 times with Amicon Ultra 50 KDa MWCO centrifugal filter (Millipore) and stored in PBS solution at 4° C.

For antibody-ssDNA conjugation with Thunder-Link oligo conjugation system, IgG was diluted to 1 mg/mL in 100  $\mu$ L PBS, activated by the Antibody Activation Reagent for 1 Hr at RT, and purified using desalting column. At the same time, 5' amine-terminated ssDNA oligonucleotides were diluted to 80  $\mu$ M in 100  $\mu$ L PBS, activated by the Oligo Activation Reagent for 1 Hr at RT, and desalted. Activated IgG and ssDNA were mixed at a volume ratio of 2:1 (200  $\mu$ L IgG+100  $\mu$ L ssDNA+100  $\mu$ L wash buffer), reacted overnight at RT, and stored at 4° C. For optimization studies, following IgG:ssDNA volume ratios were tested: 50+50, 50+30, 50+20, and 50+10.

#### QDot-ssDNA Conjugation.

Amine-functionalized PEG-coated QDots (Qdot ITK amino (PEG) quantum dots, Invitrogen) with emission peaks centered at 525, 545, 565, 585, 605, and 655 nm were used for the preparation of QDot-ssDNA probes. Amine-terminated HPLC purified 16nt-long ssDNA tags were purchased from IDT DNA (see TABLE 5, Tag IDs 1A-6A). Oligonucleotides were activated with bifunctional cross-linker BS3 (Bis[sulfosuccinimidyl] suberate, Thermo Scientific), followed by covalent conjugation with QDots. 100  $\mu$ L 40  $\mu$ M ssDNA solution in PBS was mixed with 500 molar excess of BS3 and incubated for 30 minutes at room temperature. Excess crosslinker was removed by 3 rounds of desalting in Zeba desalting spin columns (Thermo Scientific) pre-washed with PBS. Activated ssDNA was then mixed with 25  $\mu$ L 8  $\mu$ M stock QDot solution. The reaction was incubated overnight at room temperature and purified by ultrafiltration for at least 6 times with Amicon Ultra 100 KDa MWCO centrifugal filter (Millipore). Purified QDot-ssDNA probes were stored in PBS solution at 4° C.

Agarose gel electrophoresis was used for characterization of QDot-ssDNA probes. Procedure was performed on a 2% agarose gel in 1 $\times$ TBE at 90V for 2 hrs.

#### Cell Culture and Processing.

Human cervical cancer cell line HeLa (ATCC) was used as a model specimen for evaluation of the multi-omics imaging via DNA encoding. Cells were grown in glass-bottom 24-well plates (Greiner Bio-One) in a humidified atmosphere at 37° C. with 5% CO<sub>2</sub> to a density of 80-90% using MEM culture medium with L-glutamine (Gibco) supplemented with 10% fetal bovine serum (Gibco). Prior to labeling, cells were rinsed with PBS, fixed with 4% formaldehyde in PBS for 5 min at room temperature followed by 15 min at 4° C., permeabilized with ice-cold 0.5% TritonX-100 (Thermo Scientific) in PBS for 15 min at 4° C., and washed with PBS. For mRNA imaging, cells were immediately processed for in situ hybridization to minimize degradation of mRNA prior to labeling. For protein imaging only, fixed cells could be stored in PBS with 0.03% sodium azide at 4° C. for several days.

#### Encoding Via Immunorecognition.

Encoding of protein targets in formalin-fixed cells was performed via incubation with antibody-ssDNA bioconjugates. Prior to labeling, cells were blocked by 2% BSA (from 10% BSA/PBS solution, Thermo Scientific), 0.5% Western blot blocking reagent (from 10% solution, Roche), 0.1% low MW dextran sulfate (9-20 kDa MW, Sigma-Aldrich), 0.1 mg/mL shredded salmon sperm DNA (Invitrogen), and 1 $\times$ PBS for 30 min at RT. Antibodies were used at a final concentration of 5  $\mu$ g/mL diluted in 2% BSA, 0.1% dextran sulfate, 0.1 mg/mL shredded salmon sperm DNA, and 1 $\times$ PBS and incubated with cells for 1-2 hrs at RT. Following labeling, cells were washed with PBS.

For reference studies, cell labeling with unmodified antibodies was performed in a similar fashion.

#### Encoding Via In Situ Hybridization (ISH).

Encoding of mRNA targets was performed via hybridization with ssDNA-tagged mRNA ISH probes. Cells were equilibrated with 10% formamide (Thermo Scientific), 2 mM RVC (New England BioLabs), 2 $\times$ SSC (Invitrogen) buffer for 30 min at RT and then incubated with 400  $\mu$ L/well 250 nM mix of mRNA ISH probes in 1% dextran sulfate (>500 kDa MW, Sigma-Aldrich), 1 mg/mL tRNA (from *E. coli*, Roche), 10% formamide, 2 mM RVC, 2 $\times$ SSC hybridization buffer for 4 Hrs (or overnight) at 37° C. Following hybridization, cells were washed with warm 10% formamide, 2 $\times$ SSC buffer for 30 min at 37° C., two changes of 1 $\times$ PBS for 10 min at RT, and blocked by 2% BSA, 0.5% Western blot blocking reagent, 0.1% low MW dextran sulfate, 0.1 mg/mL shredded salmon sperm DNA, 1 $\times$ PBS for 30 min at RT.

#### Encoding for Multi-Omics Studies.

Encoding of protein and mRNA targets on the same specimen was performed by combining immunorecognition and in situ hybridization procedures. First, cells were hybridized with ssDNA-tagged mRNA ISH probes as described above. Following hybridization and washing, cells were blocked, incubated with antibody-ssDNA bioconjugates for 1-2 Hrs at RT, and washed with PBS.

#### Specimen Labeling with QDot Probes.

Following encoding of targets with ssDNA tags, cells were simultaneously labeled with complementary QDot-ssDNA' probes. QDots were used at a final concentration of 5 nM in 2% BSA, 0.1% low MW dextran sulfate, 0.1 mg/mL shredded salmon sperm DNA, 1 $\times$  PBS and incubated with cells for 2-4 Hrs at RT. Following staining cells were washed with PBS. Optionally, nuclei could be counter-stained by a 5-min incubation with DAPI.

For reference immunofluorescence studies, cell staining with QDots functionalized with secondary Ab fragments

(Qdot goat F(ab')<sub>2</sub> anti-mouse or anti-rabbit IgG conjugates (H+L), Invitrogen) was performed in a similar fashion.

RNAi.

Knock-down of GAPDH expression was done via cell transfection with GAPDH siRNA (Ambion). For forward transfection, cells were grown in a glass-bottom 24-well plate overnight and then treated with 500  $\mu$ l/well culture medium containing 25 nM GAPDH siRNA and 0.5  $\mu$ l/well DharmaFECT-2 transfection reagent (Dharmacon) for 24 hrs. For reverse transfection, cells were grown in a 10 cm TC-treated dish, trypsinized, mixed in suspension with culture medium containing 25 nM GAPDH siRNA and 0.5  $\mu$ l/well DharmaFECT-2 transfection reagent, seeded into a glass-bottom 24-well plate at 500  $\mu$ l/well cell suspension, and incubated for 24 hrs or 48 hrs. Following transfection, cells were processed for staining. Triplicate samples were also prepared for RT-PCR analysis.

RT-PCR Analysis.

Total RNA was isolated from cell pellets using TRIzol reagent (Invitrogen) according to the manufacturer's protocol. Two hundred nanograms of RNA was converted to cDNA using random hexamer primer and MultiScribe Reverse Transcriptase Reagent (Applied Biosystems). One hundred nanograms of cDNA was amplified by the Real-Time PCR using SensiFAST™ Real-Time PCR Kits (Bio-line, UK) on Chromo4 Real-Time PCR detection system (Bio-Rad). The primers used for GAPDH amplification were 5'-TCGCTCTCTGCTCCTCCTGTTC-3' (forward primer; SEQ ID NO: 1033) and 5'-CGCCCAATACGACCAAATCC-3' (reverse primer; SEQ ID NO: 1034). Cyclophilin A (PPIA) was used as an internal control, and the primers were 5'-GTCAACCCACCGTGTCTTC-3' (forward primer; SEQ ID NO: 1035) and 5'-TTTCTGCTGTCTTTGGGACCTTG-3' (reverse primer SEQ ID NO: 1036). To confirm the PCR specificity, PCR products were subjected to a melting-curve analysis. The comparative threshold (CO method) was used to calculate the relative mRNA amount of the treated sample in comparison to control samples. Mean value from triplicate samples was reported.

Imaging and Signal Analysis.

IX-71 inverted fluorescence microscope (Olympus) equipped with a true-color CCD (QColor5, Olympus) and a hyperspectral imaging camera (Nuance, 420-720 nm spectral range, CRI, now PerkinElmer) was used for cell imaging. Low-magnification images were obtained with  $\times$ 20 dry objective (NA 0.75, Olympus) and high-magnification with  $\times$ 40 (NA 1.30, Olympus) and  $\times$ 100 (NA 1.40, Olympus) oil-immersion objectives. Wide UV filter cube (330-385 nm band-pass excitation, 420 nm long-pass emission, Olympus) was used for imaging of all QDot probes, while Rhodamine LP cube (530-560 nm band-pass excitation, 572 nm long-pass emission, Chroma) was used for Alexa Fluor 555 detection. All images were acquired with cells attached to the coverslip bottom of the well and immersed in PBS without use of anti-fading reagents.

Nuance image analysis software was used to unmix the obtained multispectral images based on the reference spectra of each QDot component along with an extra channel for background fluorescence. In a false-color composite image, brightness and contrast of each channel was automatically adjusted for best visual representation and clear depiction of relative target distribution, unless noted otherwise. For direct comparison of QDot staining intensity individual QDot channels were normalized.

DNA Encoding for Multi-Omic Imaging Studies.

To demonstrate the DNA encoding for multi-omics imaging studies concurrent analysis of single-cell molecular expression profiles at mRNA and protein levels were performed. Fluorescent quantum dot probes (QDots) in combination with fluorescence microscopy and hyperspectral imaging (HSI) were employed for simultaneous visualization of all ssDNA tags following separate encoding of mRNA and protein targets (FIG. 5A). For example, GAPDH and HSP90-alpha mRNA molecules and their respective product proteins can be readily labeled by 4-color QDots to highlight relative intracellular distribution and abundance of the two target types at a single-cell level (FIG. 5B). Unlike direct labeling procedures performed at a single incubation condition fixed for all targets and probes, DNA encoding enables tuning of conditions to favor recognition of individual target types and hybridization with detection probes in separate steps, offering great flexibility in choice of specimens, targets, and imaging systems (FIG. 6).

QDot-Based Multi-Omics Imaging Platform.

To implement and systematically characterize the model QDot-based multi-omics imaging platform, a set of 6 unique 16 bp ssDNA/ssDNA' linkers was developed for encoding of up to 6 different molecular targets (TABLE 4) along with a library of complementary 6-color QDot-ssDNA probes (FIG. 7A and FIG. 7B) and a control set of 6 secondary antibody-ssDNA (2' Ab-ssDNA) bioconjugates (FIG. 8A and FIG. 8B). Indirect labeling of  $\beta$ -tubulin in HeLa cells via a 3-step procedure involving incubation with unmodified primary antibodies, 2' Ab-ssDNA bioconjugates, and complementary QDot-ssDNA' probes demonstrated preserved antigen-recognition functionality of ssDNA-modified antibodies and high specificity of QDot staining via DNA hybridization (FIG. 9).

Multiplex Protein Immuno-Labeling.

Multiplexed protein immuno-labeling was realized through preparation of a library of primary antibody-ssDNA (1' Ab-ssDNA) bioconjugates (FIG. 10A, FIG. 10B, and FIG. 10C; and FIG. 11A, FIG. 11B, FIG. 11C, FIG. 11D, and FIG. 11E). Characterization of such bioconjugates with PAGE and cell staining confirmed preserved stability and antigen-binding functionality of antibodies, specificity of target staining with QDots in a 2-step procedure, and consistent target identification with different QDot colors in a multiplexed imaging format (FIG. 11A, FIG. 11B, FIG. 11C, FIG. 11D, and FIG. 11E). Nuclear envelope protein Lamin A, microtubule  $\beta$ -tubulin, and cytoplasmic proteins HSP90-alpha and GAPDH were labeled as model target molecules with distinct characteristic intracellular localization.

Labeling of model GAPDH and HSP90-alpha mRNA molecules via an indirect in situ hybridization (ISH) procedure was done with modified mRNA ISH oligonucleotide probes featuring 5' 20 nt mRNA-recognition portion and a 3' 16 nt QDot-binding tag separated by a single-stranded AAAAA spacer (TABLE 5 and TABLE 6). Hybridization of oligonucleotide probes under optimized ISH conditions yielded labeling of each mRNA molecule with multiple ssDNA tags (up to 36 for GAPDH and 48 for HSP90-alpha), producing distinct spots upon staining with complementary QDot-ssDNA probes consistent with results achieved with conventional mRNA ISH protocols (FIG. 12). In some instances, non-complementary QDot-ssDNA probes failed to hybridize to exposed ssDNA tags, producing minimal non-specific staining background. To explore effects of potential secondary structure formation in 41 nt ssDNA oligonucleotides as well as steric hindrance experienced by QDots approaching tightly spaced ssDNA tags, an alternative mRNA ISH probe set was designed with each probe

containing a 16 bp dsDNA spacer between 5' mRNA-recognition and 3' QDot-binding portions. Indeed, physical separation of functional ssDNA portions improved mRNA staining intensity in comparison to linear 41 nt ssDNA oligonucleotides (FIG. 13A, FIG. 13B, FIG. 13C, and FIG. 13D), offering one strategy for enhancing per-spot signal intensity and improving signal-to-noise ratio.

Separation of target-recognition and QDot-labeling events via an intermediate DNA encoding enabled straightforward implementation of a model multi-omics imaging protocol, with both mRNA and protein targets being robustly labeled by respective QDot probes and accurately identified through hyperspectral imaging and analysis (FIG. 14), corroborating broad applicability of the DNA encoding strategy for simultaneous detection and imaging of various types of targets within the same specimen.

Multi-omics imaging platform was then applied to study gene knock-down via RNAi at a single-cell level. HeLa cells were transfected with GAPDH-targeting siRNA (as well as non-targeting siRNA for control) for 24 hrs, and GAPDH mRNA abundance was assessed with RT-PCR and QDot-based imaging. In some cases, bulk GAPDH mRNA measurement by RT-PCR indicated silencing efficiency of 78% with forward transfection and 95% with reverse transfection. At the same time, imaging revealed heterogeneity in RNAi, likely resulting from heterogeneous cell transfection with siRNA throughout different regions of cell culture. For example, forward transfection failed to achieve efficient GAPDH mRNA degradation in dense cell populations, yielding areas of completely silenced cells along with patches of cells with normal GAPDH mRNA expression levels (FIG. 15). In contrast, reverse transfection achieved a more uniform cell transfection in suspension, producing a greater proportion of silenced cells with only a few wild-type clones (FIG. 16). Direct comparison of mRNA imaging results obtained from forward vs. reverse transfection further corroborated complete mRNA degradation upon successful transfection with either method along with unperturbed GAPDH mRNA levels in non-transfected cells (FIG. 17), suggesting an all-on/all-off mode of GAPDH RNAi and attributing incomplete silencing observed with bulk RT-PCR analysis to heterogeneity in siRNA transfection.

Selectivity of GAPDH RNAi was confirmed by performing dual-target imaging of GAPDH mRNA and HSP90-alpha mRNA. Target-selective siRNA should trigger degradation of only its complementary target mRNA, having no immediate effect on non-targeted mRNA molecules. This was indeed observed with GAPDH RNAi studies (FIG. 18). Indirect dual-target ISH produced robust staining of both mRNA species in reference HeLa cells grown in culture

medium. Similarly, cell transfection with non-targeting control siRNA failed to produce any effect on mRNA expression. Transfection with GAPDH-targeting siRNA, however, triggered rapid degradation of GAPDH mRNA within 24 hrs post-transfection, while leaving non-targeted HSP90-alpha mRNA intact. A single non-transfected cell within the field of view features intact expression of both GAPDH and HSP90 mRNA, consistent with discussion above.

Imaging of mRNA unambiguously demonstrated heterogeneity in RNAi stemming from incomplete cell transfection with siRNA. However, such heterogeneity could not be detected at the protein level, as GAPDH protein remained unperturbed 24 Hrs post-transfection in both transfected and non-transfected cells, as was evident from dual labeling of GAPDH mRNA and protein (FIG. 19). To further investigate the disparity between RNAi effect at mRNA and protein levels, HeLa cells were reverse transfected with GAPDH-targeting siRNA for 24 and 48 Hrs and processed for multiplexed imaging of GAPDH and HSP90-alpha mRNA and their respective protein products. Consistent with studies discussed earlier, 24 Hrs post-transfection a complete degradation of GAPDH mRNA was observed, whereas GAPDH protein level remained unperturbed (FIG. 20A). In contrast, 48 hrs post-transfection a substantial reduction of GAPDH protein level could be observed, with GAPDH mRNA remaining below the detection limit (FIG. 20B). HSP90 mRNA and protein levels remained unperturbed through 48 hours, confirming selectivity of GAPDH silencing. Further, all molecular targets exhibited consistent unperturbed levels in reference non-transfected cells (FIG. 21A and FIG. 21B) and cells transfected with non-targeting siRNA (FIG. 22A and FIG. 22B) throughout the study, corroborating that the observed GAPDH knock-down indeed resulted from RNAi mechanism. Multiplexed analysis was fully confirmed by a series of single-plex studies to mitigate any artifacts that could potentially be introduced from the multi-omics labeling methodology, HSI, and image analysis (FIG. 23A and FIG. 23B).

In some cases, delay in RNAi effect at the protein level is present, as proteins are typically degraded and cleared slower in comparison to siRNA-mediated mRNA degradation. In other cases, heterogeneity in cell transfection can modulate assessing RNAi efficiency with bulk RT-PCR measurement and downstream phenotypic and molecular signaling analysis. Non-transfected cells might gain growth advantage and achieve substantial clonal expansion during the time it takes for higher-level manifestations of RNAi to occur, thus distorting observed RNAi effect at a population level. Imaging-based analysis at a single-cell level can by-pass this ambiguity and can offer a more accurate insight into molecular processes.

TABLE 4

List of ssDNA/ssDNA' taq pairs for encoding of molecular targets			
Tag ID		Sequence*	SEQ ID NO:
QDot-coupled	1A	5' - /5AmMC6/iSp18/CGTCGCACCAAGAAAT-3'	936
	2A	5' - /5AmMC6/iSp18/TAGACTTGCCATACGT-3'	937
	3A	5' - /5AmMC6/iSp18/AATTCTTGAGACCAGG-3'	938
	4A	5' - /5AmMC6/iSp18/ATCTGCCCAAACCTCCA-3'	939
	5A	5' - /5AmMC6/iSp18/TCCCAAGCGTCATCT-3'	940
	6A	5' - /5AmMC6/iSp18/TCTATCGGACGCTGTA-3'	941

TABLE 4-continued

List of ssDNA/ssDNA' tag pairs for encoding of molecular targets			
Tag ID	Sequence*	SEQ ID NO:	
IgG-coupled	1B 5' - /5AmMC6 /AAAAAAAAAATTTCTTGGTGCAGC-3'	942	
	2B 5' - /5AmMC6 /AAAAAAAAAACGTATGGCAAGTCTA-3'	943	
	3B 5' - /5AmMC6 /AAAAAAAAACCTGGTCTCAAGAATT-3'	944	
	4B 5' - /5AmMC6 /AAAAAAAAATGGAGTTTGGGCAGAT-3'	945	
	5B 5' - /5AmMC6 /AAAAAAAAAAGATGACGCTTGGGAA-3'	946	
	6B 5' - /5AmMC6 /AAAAAAAAATACAGCGTCCGATAGA-3'	947	

\*all ssDNA tags have 5' terminal amine group (/5AmMC6/) for bioconjugation separated from the pairing sequence by either a hexa-ethyleneglycol spacer (/iSp18/) for QDot-coupled tags or 10A oligonucleotide spacer (AAAAAAAA; SEQ ID NO: 1037) for IgG-coupled tags.

TABLE 5

Sequences of GAPDH mRNA ISH probes (with 2B encoding tag)			
#	mRNA-recognition region	encoding tag 2B	SEQ ID NO:
1	5' - ATTTATAGAAACCGGGGCC	AAAAAAAAACGTATGGCAAGTCTA-3'	948
2	5' - CGAACAGGAGGAGCAGAGAG	AAAAAAAAACGTATGGCAAGTCTA-3'	949
3	5' - GCTGGCGACGCAAAAGAAG	AAAAAAAAACGTATGGCAAGTCTA-3'	950
4	5' - CATGGTGTCTGAGCGATGT	AAAAAAAAACGTATGGCAAGTCTA-3'	951
5	5' - TACGACCAATCCGTTGACT	AAAAAAAAACGTATGGCAAGTCTA-3'	952
6	5' - CAGAGTTAAAAGCAGCCCT	AAAAAAAAACGTATGGCAAGTCTA-3'	953
7	5' - GGGTCATTGATGGCAACAAT	AAAAAAAAACGTATGGCAAGTCTA-3'	954
8	5' - AACCATGTAGTTGAGGTCA	AAAAAAAAACGTATGGCAAGTCTA-3'	955
9	5' - GGGTGAATCATATTGGAA	AAAAAAAAACGTATGGCAAGTCTA-3'	956
10	5' - TTGACGGTGCCATGGAATT	AAAAAAAAACGTATGGCAAGTCTA-3'	957
11	5' - CATTGATGACAAGCTTCCC	AAAAAAAAACGTATGGCAAGTCTA-3'	958
12	5' - TCCTGGAAGATGGTGATGG	AAAAAAAAACGTATGGCAAGTCTA-3'	959
13	5' - CCACTTGTATTTGGAGGGAT	AAAAAAAAACGTATGGCAAGTCTA-3'	960
14	5' - GGACTCCACGACGTACTCAG	AAAAAAAAACGTATGGCAAGTCTA-3'	961
15	5' - TTCTCCATGGTGGTGAAGA	AAAAAAAAACGTATGGCAAGTCTA-3'	962
16	5' - AGAGATGATGACCCTTTTG	AAAAAAAAACGTATGGCAAGTCTA-3'	963
17	5' - GACGAACATGGGGCATCAG	AAAAAAAAACGTATGGCAAGTCTA-3'	964
18	5' - CATACTTCTCATGGTTCAC	AAAAAAAAACGTATGGCAAGTCTA-3'	965
19	5' - ATTGCTGATGATCTTGAGGC	AAAAAAAAACGTATGGCAAGTCTA-3'	966
20	5' - CTAAGCAGTTGGTGGTGCA	AAAAAAAAACGTATGGCAAGTCTA-3'	967
21	5' - CCACGATACCAAAGTTGTC	AAAAAAAAACGTATGGCAAGTCTA-3'	968
22	5' - TCTTCTGGTGGCAGTGATG	AAAAAAAAACGTATGGCAAGTCTA-3'	969
23	5' - TAGAGGCGAGGATGATGTT	AAAAAAAAACGTATGGCAAGTCTA-3'	970
24	5' - TCAGCTCAGGGATGACCTT	AAAAAAAAACGTATGGCAAGTCTA-3'	971
25	5' - CACTGACACGTTGGCAGTGG	AAAAAAAAACGTATGGCAAGTCTA-3'	972
26	5' - CAGTTTTTCTAGACGGCAG	AAAAAAAAACGTATGGCAAGTCTA-3'	973

TABLE 5-continued

Sequences of GAPDH mRNA ISH probes (with 2B encoding tag)			
#	mRNA-recognition region	encoding tag 2B	SEQ ID NO:
27	5'-CACCTTCTTGATGTCATCAT <b>AAAAA</b> ACGTATGGCAAGTCTA-3'		974
28	5'-GCTGTTGAAGTCAGAGGAG <b>AAAAA</b> ACGTATGGCAAGTCTA-3'		975
29	5'-CGTCAAAGGTGGAGGAGTGG <b>AAAAA</b> ACGTATGGCAAGTCTA-3'		976
30	5'-AGTGGTCGTTGAGGGCAAT <b>AAAAA</b> ACGTATGGCAAGTCTA-3'		977
31	5'-TCATACCAGGAAATGAGCTT <b>AAAAA</b> ACGTATGGCAAGTCTA-3'		978
32	5'-CCTGTTGCTGTAGCCAAAT <b>AAAAA</b> ACGTATGGCAAGTCTA-3'		979
33	5'-TGAGGAGGGGAGATTCACT <b>AAAAA</b> ACGTATGGCAAGTCTA-3'		980
34	5'-CTCTTCAAGGGTCTACAT <b>AAAAA</b> ACGTATGGCAAGTCTA-3'		981
35	5'-TACATGACAAGGTGCGGCTC <b>AAAAA</b> ACGTATGGCAAGTCTA-3'		982
36	5'-TGAGCACAGGTTACTTTAT <b>AAAAA</b> ACGTATGGCAAGTCTA-3'		983

## Note:

mRNA-recognition region and encoding tag are separated by a spacer (bolded and italicized). Shorter 41nt mRNA ISH probes contain -AAAA- single-stranded spacer. Longer 60nt mRNA ISH probes contain pre-hybridized 16bp double-stranded spacer flanked by -AAAA- single-stranded linkers.

TABLE 6

Sequences of HSP90-alpha mRNA ISH probes (with 4B encoding tag)			
#	mRNA-recognition region	encoding tag 4B	SEQ ID NO:
1	5'-AGGAGTATGATTGTCAACCC <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		984
2	5'-CCTATATAAGGCGAAGCAC <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		985
3	5'-GAGTGACTCGAGAGAGCTAC <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		986
4	5'-ATAGTGAGCAACGTAGGCTT <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		987
5	5'-GGACATGAGTTGGCAATT <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		988
6	5'-GAGATCAACTCCCGAAGGA <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		989
7	5'-AATCTTGTCCAAGGCATCAG <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		990
8	5'-AACTTCGAAGGTCTGTCA <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		991
9	5'-GGTTGGGGATGATGTCAAT <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		992
10	5'-TACCAAAGTCAGGGTACGTT <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		993
11	5'-TGAGATCAGCTTGGTCAT <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		994
12	5'-TTGGCAATGGTTCCCAAAT <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		995
13	5'-CTGAAGAGCCTCCATGAAT <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		996
14	5'-CCACCAAGTAGGCAGAATA <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		997
15	5'-TGCTTTGTGATCACAACC <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		998
16	5'-CAGAAGACTCCCAAGCATA <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		999
17	5'-AGCACGCACAGTGAAGGA <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		1000
18	5'-TCTAGGTACTCTGTCTGAT <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		1001
19	5'-TAAAGGTGATGGGATAGCC <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		1002
20	5'-TGTTTAGTCTTCTCTGAT <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		1003
21	5'-AGGGTTTCTGGTCCAAAT <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		1004
22	5'-TCATTAGTGAGGCTCTTGT <b>AAAAAT</b> GGAGTTTGGGCAGAT-3'		1005

TABLE 6-continued

Sequences of HSP90-alpha mRNA ISH probes (with 4B encoding tag)			
#	mRNA-recognition region	encoding tag 4B	SEQ ID NO:
23	5'-AAAGTGCTTACTGCTGCAAGT <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1006
24	5'-TGAATTCCTCACTGACCTTCT <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1007
25	5'-GAGCCCACGACGGAATAAA <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1008
26	5'-TGAACACACGGCGGACATAG <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1009
27	5'-ATCAACTCATCACAGCTGT <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1010
28	5'-AAGATTTTGCTCTGCTGGAG <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1011
29	5'-AGAGAAGAGCTCAAGGCAC <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1012
30	5'-GTGGATTCCAGCTTGAGAT <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1013
31	5'-AGACTGGGAGGTATGATAGC <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1014
32	5'-CTCTGACAGAGATGTCATC <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1015
33	5'-TAGATGGACTTCTGTGTCT <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1016
34	5'-GCTCCACAAAAGCTGAGTT <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1017
35	5'-CATATATACCACCTCGAAGC <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1018
36	5'-ACACAGTACTCGTCAATGGC <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1019
37	5'-TTCCCATCAAATCCTTGAG <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1020
38	5'-GAGATTGTCACCTTCTCA <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1021
39	5'-TGCAGCAAGGTGAAGACAC <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1022
40	5'-GCTTTTGGCCATCATATAG <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1023
41	5'-AACTGCCTTATCATTCTT <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1024
42	5'-ATCCTCAAGGAAAAGCCAG <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1025
43	5'-TGATCATGCGATAGATGCG <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1026
44	5'-CATCAGGAAGTGCAGCATT <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1027
45	5'-CAAGGGCACAGTTTTCC <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1028
46	5'-TACTGCCTTCAACACAAG <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1029
47	5'-AGAGTAGAGAGGAATGGG <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1030
48	5'-TACACAACATCCAATCCTG <b>AAAAA</b> TGGAGTTTGGGCAGAT-3'		1031

Note:  
mRNA-recognition portion and encoding tag are separated by a spacer (bolded and italicized). Shorter 41nt mRNA ISH probes contain -AAAAA- single-stranded spacer. Longer 60nt mRNA ISH probes contain pre-hybridized 16bp double-stranded spacer flanked by -AAAA- single-stranded linkers.

Example 3

Global In Situ Visualization of the DNaseI Hypersensitivity Site (DHS) Compartment of a Cell

This example shows the global in situ visualization of the DNaseI Hypersensitivity Site (DHS) compartment of a cell, which allows for identification of nuclear compartments where regulatory DNA activation occurs. As shown in the graphic on the left side of FIG. 24, K562 cells were fixed with Paxgene reagent, treated with DNaseI, DNaseI-induced nicks were labeled using terminal transferase (TdT) and ethynyl-dUTP (EdUTP) (TUNEL assay), Alexafluor-488 (AF488) was conjugated to the EdUTP via copper click

chemistry, and then SPDM imaging was performed. FIG. 24 shows multiple images of this. The top left image is of the raw signal data. The local density map image (top middle) shows a ring of condensation at the nuclear lamina, which is similar to findings reported by the Weintraub lab 30 years ago (Weintraub, Cell (1985) 43:471-482); see FIG. 24 top right reproduced image). Approximately 18.4% of the localized points are within the ring density at the nuclear lamina, as shown the calculations in the lower right box, in which the image data calculation was based off the image on the lower left of FIG. 24. The image data calculation is similar to the proportion of K562 DHS within lamina-associated domains (LADS). These findings indicate labeling of DNaseI cut sites

in a cell's nucleus using a TUNEL assay may be used for better understanding of the nuclear localization of regulatory DNA activation.

#### Example 4

##### Nano-FISH Methods

This example shows how nano-FISH was used to detect the presence or absence of the locus control region in human erythroleukemia K562 cells.

##### Cells and Tissue Culture

Human erythroleukemia K562 cells and their derivative lacking the locus control region ( $\Delta$ LCR) were maintained in RPMI 1640 media supplemented with 2 mM L-glutamine (0.3 g/L), 10% Fetal Bovine Serum, penicillin, and streptomycin at 37° C. in 5% CO<sub>2</sub>.

##### In Silico Design of Nano-FISH Probe Pools

Tiled 40 bp probe pools with a minimum of 2 bp spacing between consecutive probes were designed using Primer3 with default parameters. The resulting tiled probe sets were compared to a 16-mer database of genomic sequences in each register to model partial matches of probes to genomic sequences that could result in inappropriate background staining. A uniquely mapping oligonucleotide would therefore have a total of 24 matches to the 16-mer database. Individual probe sets with >100 16-mer database matches were empirically discarded from consideration. For the genomic target regions examined in this study, a pool of at least 30 oligonucleotides that satisfied these design criteria was used.

##### Nano-FISH Protocol

Cells were harvested, washed once in phosphate buffered saline (PBS), re-suspended in a small volume of PBS and subsequently seeded on 18 mm×18 mm coverslips in a 6-well plate that had been coated with poly-L-lysine (Sigma P1399). After allowing cells to adhere for 5 to 10 minutes at room temperature they were fixed by the addition of 4% formaldehyde (Polysciences 18814-10) in PBS for 10 minutes, washed with PBS, and then permeabilized for 15 minutes with 0.5% Triton X-100 in PBS. Following two washes in PBS, the cells were subjected to a 5 minute treatment of 0.1 M HCl and subsequently washed twice in saline sodium citrate (2×SSC) before incubation with RNase A (25 ug/mL in 2×SSC) at 37° C. for 30 minutes. The cover slips were washed in 2×SSC again and then pre-equilibrated for at least one hour in 50% formamide (Amresco 0606), 2×SSC (pH 7.0) at room temperature. To denature the cellular DNA the cover slips were incubated for 4.5 minutes in 70% formamide, 2×SSC (pH 7.0) preheated to 78° C. in a 6-well plate on a heat block equipped with an aluminum block designed for tissue culture plates. For consistency, only the center two wells were used for denaturations and the temperature allowed to re-equilibrate before the next batch. Cover slips were then inverted onto 80  $\mu$ l of hybridization solution (50% formamide, 10% dextran sulfate, 2×SSC, 250 pM oligonucleotide pool) on parafilm in a humid chamber and incubated overnight at 37° C. Post-hybridization washes included two 15 minute incubations in 2×SSC followed by two 7 minute washes in 0.2×SSC/0.2% Tween-20 at 56° C. on a heat block and one wash in 4×SSC/0.2% Tween-20 at room temperature. Cellular DNA was counterstained with DAPI (100 ng/mL in 2×SSC), followed by two more washes in 2×SSC. Cover slips were then mounted on slides for imaging with Prolong Gold (Molecular Probes P36930).

##### Imaging

For standard widefield microscopy, slides were imaged on an inverted Nikon Eclipse Ti widefield microscope with a 60× Nikon Plan Apo lambda NA 1.40 oil objective and an Andor Zyla 4.2CL10 CMOS camera.

#### Example 5

##### Nano-FISH Detection of a 1.8 kb Nucleic Acid Sequence

This example and FIG. 33 shows the use of Nano-FISH to detect a 1.8 kb nucleic acid sequence. FIG. 33A shows a schematic of a Nano-FISH experiment. FIG. 33B shows the application of the Nano-FISH strategy to detect a 1.8 kb region encompassing the HS2 hypersensitive site of the  $\beta$ -globin locus control region (LCR) in triploid K562 erythroleukemia cells. FIG. 33C shows colocalization of the Nano-FISH signals (~1.8 kb target region) with those from standard BAC-derived probes (conventional DNA-FISH; ~170 kb target region), confirming the specificity of the detected Nano-FISH signal. Compared to the large size of BAC probes used to detect the  $\beta$ -globin LCR, Nano-FISH probes targeting HS2 covered a target region that was approximately 2 orders of magnitude smaller in size. Although most, but not all spots corresponding to the alleles in the triploid cell, were consistently detected using 30 tiled 40 bp oligonucleotide probes targeting the HS2 hypersensitive site, increasing the number of probes and expanding the corresponding labeled genomic DNA target region, Nano-FISH was shown to be tunable. A modest increase in the number of probes (~90), the frequency of allele detection by Nano-FISH matches the performance of the BAC-probe based golda performance benchmark of Nano-FISH versus standard BAC probes. Conversely, decreasing the number probes below 30 drastically reduced allele detection sensitivity. Therefore, as shown in FIG. 33D, the sensitivity of efficiency and resolution of detection using Nano-FISH may be tuned according to the number of probes being used.

Using an efficient and robust automated image processing pipeline, results from hundreds of cells across multiple replicates were quantified. These studies showed that the diffraction-limited signals produced by Nano-FISH were smaller and dimmer than those generated by BAC-based probes (FIG. 33E and FIG. 33E). Despite this, Nano-FISH still showed robust detection of genomic regions with varying size, such as genomic region size ranging from about 800 bp to 2.1 kb, as shown if FIG. 33G. Thus, Nano-FISH is able to successfully label endogenous non-repetitive DNA loci that are much smaller than the current limit of resolution of BAC- and fosmid-based DNA-FISH approaches.

#### Example 6

##### Fine Structural Analysis Using Nano-FISH

This example and FIG. 34 show the use of Nano-FISH to perform fine structural analysis of specific genomic loci within the nucleus. Probe pools were designed to target a 1.6 kb region of chromosome 19 and a 1.4 kb region of chromosome 18. These chromosomes were chosen since chromosome 19 is known to occupy a central position within the nucleus while chromosome 18 is more marginally located. FIG. 34A shows the distinct spots produced by Nano-FISH probes targeting specific loci on these chromosomes. To measure the relative localization of the detected loci, the relative radial distance (RRD), a normalized measure of the position of the detected spot with respect to the

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nuclear centroid, was calculated. FIG. 34B shows a schematic of the relative radial distance. FIG. 34C shows that the chromosome 18 Nano-FISH signals are closer to the nuclear periphery. The distributions were obtained across 2,396 chromosome 18 signals and 3,388 chromosome 19 signals. FIG. 34D shows radial histograms of the two target loci. The differences in the distribution of signals with respect to the nuclear centroid are readily apparent in the histograms.

## Example 7

Examination of Enhancer-Promoter Interactions  
Using Nano-FISH

This example and FIG. 35 show the use of Nano-FISH for examining the interaction of a gene enhancer with its target gene promoter. The positioning of a known enhancer of the CCND1 gene in 786-O and MCF-7 cells was examined. Based on DNaseI hypersensitivity mapping, this enhancer is active in 786-O cells, but is inactive in MCF-7 cells. Using large (~225 kb) probes, others have demonstrated that this enhancer is located in proximity to the CCND1 gene promoter in 786-O cells, but not in MCF-7 cells. Nano-FISH probes targeting the enhancer and promoter were designed and synthesized. FIG. 35A shows two-color Nano-FISH in 786-O and MCF-7 cells. The normalized inter-spot distance (NID) between these two genomic loci were compared. FIG. 35B shows a schematic of the normalized inter-spot distance. FIG. 35C shows that, on average, the spots are situated closer together in 786-O cells compared to MCF-7 cells. FIG. 35D shows that, in spite of this, absolute colocalization (NID=0) was actually a rare event in both cell types. Thus, the small size of genomic regions targeted by Nano-FISH permits fine scale localization of regulatory DNA regions and provides a granular view of their spatial localizations within nuclei.

## Example 8

Detection of Small Genomic Structural Variations  
Using Nano-FISH

This example and FIG. 36 show the use of Nano-FISH to detect small genomic structural variations such as small losses or gains of DNA. ZFN-mediated genome editing was used to generate a triploid homozygous deletion of the  $\beta$ -globin locus control region (LCR, ~18 kb) in K562 cells, as shown in FIG. 36A. Cells imbued with this deletion are referred to as  $\Delta$ LCR. Probes targeting either the HS2 or HS3 hypersensitive sites within the deleted region were utilized to detect loss of LCR in the genome edited cells, as shown in FIG. 36B and FIG. 36C. For the converse scenario, using TALEN-mediated homology directed repair, a sequence encoding for eGFP was inserted into the AAVS1 safe harbor locus on chromosome 19, as shown in FIG. 36D. This exogenously-derived sequence was readily identified by Nano-FISH, as shown in FIG. 36E and FIG. 36F.

## Example 9

Fine Scale Genome Localization Using Nano-FISH  
and Super-Resolution Microscopy

This example and FIG. 37 show the combination of Nano-FISH and super-resolution microscopy to obtain very fine-scale genome localization. A custom automated stimulated emission and depletion (STED) microscope was uti-

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lized to efficiently acquire multiple measurements of the physical distance between the HS2 and HS3 genomic loci, which are separated by 4.1 kb of linear genomic distance. FIG. 37A shows that these closely apposed loci are readily discernible as distinct spots by STED microscopy. Pair-wise measurements of other closely situated genomic segments such as HS1-HS4 (~12 kb) and HS2-HGB2 (~25 kb) were also readily obtained and revealed non-linear compaction of the  $\beta$ -globin locus control region and the surrounding genome which contains its target genes, as shown in FIG. 37B. Importantly, the high-throughput STED microscopy approach enables calculation of the distribution of actual distances between these various loci, as shown in FIG. 37C. These results demonstrated the suitability of Nano-FISH for super-resolution STED microscopy experiments.

## Example 10

## Optimal Nano-FISH Parameters

This example and FIG. 38 show a series of experiments to determine the optimal operating parameters for a Nano-FISH experiment. FIG. 38A shows how the labeling efficiency of the Nano-FISH procedure depends on denaturation temperature. With increasing temperature, the efficiency of Nano-FISH labeling increases, until a plateau is reached at a temperature of 78° C. FIG. 38B shows that the Nano-FISH labeling procedure is repeatable across experiments. FIG. 38C shows Nano-FISH detected for genomic regions with varying size, such as genomic region size ranging from about 800 bp to 2.1 kb. FIG. 38D shows how the labeling efficiency of the Nano-FISH experiment depends on the number of oligo probes used. The labeling efficiency increases with the number of oligo probes used, attaining a maximum efficiency when 30 oligo probes are utilized. FIG. 38E shows how the detected fluorescence spot size depends on the number of oligo probes. FIG. 38F shows how the intensity of the fluorescence spot size depends on the number of oligo probes.

## Example 11

## Comparison of Nano-FISH and Conventional FISH

This example and FIG. 39 show a comparison of Nano-FISH and conventional FISH. FIG. 39A shows fluorescence images of  $\beta$ -globin lacking the LCR using conventional BAC probes (left panel), a pool of HS1-5 probes (middle panel), and the HS2 Nano-FISH technique (right panel). FIG. 39B shows the size of the probe sets used for the BAC, HS1-5, and HS2 experiments. As can be seen, the HS2 Nano-FISH experiment utilizes a significantly smaller nucleic acid sequence than conventional FISH techniques. FIG. 39C shows the labeling efficiency of the BAC, HS1-5, and HS2 experiments. FIG. 39D shows the size of the FISH spots for the BAC, HS1-5, and HS2 experiments. FIG. 39E shows the intensity of the FISH signals for the BAC, HS1-5, and HS2 experiments. As can be seen, the Nano-FISH experiment produces a lower signal-to-noise ratio (SNR) than conventional methods, with the Nano-FISH experiment producing a SNR smaller than the BAC method by a factor of approximately 2. The loss in SNR comes with a reduction in the size of the nucleic acid sequence by a factor of approximately 100. Thus, the tradeoff in SNR is well worth the significant reduction in size of nucleic acid sequence.

## Discovery of Novel Biomarkers Using Nano-FISH

This example shows the discovery of the expression of novel biomarkers that correlate the number of the target nucleic acid sequence in a cell. A sample with a population of cells that is heterogenous for the number of target nucleic acid sequences in a cell is obtained. Individual cells from the sample are distributed into a single well of a plate and are allowed to clonally expand. Samples of cells from each clone is then characterized for the number of target nucleic

acid sequences in a cell using Nano-FISH and is characterized by RNA-Seq to determine novel biomarkers that correlate with the number of target nucleic acid sequences. If a novel biomarker is found to be a surface protein, then the surface protein is used as a selectable marker/sortable marker to isolate cells with the desired number of target nucleic acid sequences from the sample.

The examples and embodiments described herein are for illustrative purposes only and various modifications or changes suggested to persons skilled in the art are to be included within the spirit and purview of this application and scope of the appended claims.

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<210> SEQ ID NO 24  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 24  
  
tctttatttt attggccaca attgaacata ggtataattt 40

<210> SEQ ID NO 25  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 25  
  
cagaagcaag ccctgatcaa ggaaaccatt cacacttgat 40

<210> SEQ ID NO 26  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 26  
  
gtggcttttg ctcaaagtga ggacgttatc agctctgccc 40

<210> SEQ ID NO 27  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 27  
  
ctttaaacia aaactaaagg cgtaaggaaa gataactact 40

<210> SEQ ID NO 28  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 28  
  
cagttgccac actttttttc actgctaaag ttcgtaatga 40

<210> SEQ ID NO 29  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 29  
  
ggcaatcaga agtatttttg ttgcttctag gtcagaatga 40

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<210> SEQ ID NO 30  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 30

ggcagcaaac ttgttaggt atgattcatc attgtctgct 40

<210> SEQ ID NO 31  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 31

ctacaaaaca atgagtctga ttacgacca cagaaatgaa 40

<210> SEQ ID NO 32  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 32

cctccacag acccaaacat gctgctgcaa atgtctcact 40

<210> SEQ ID NO 33  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 33

ggacaagcac acacatcgct gggaagatct gcaagcctcc 40

<210> SEQ ID NO 34  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 34

taaacctgga taacaagaac actgtttcca ctgcgctagt 40

<210> SEQ ID NO 35  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 35

tcatcacgat gacaatggac aagccatc cctaacaggg 40

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<210> SEQ ID NO 36  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 36  
  
 tttccatgac accaggaccg taaagcacct tttacaccgt 40

<210> SEQ ID NO 37  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 37  
  
 aattgggatg tgcaaacct cttaacttgt agcaccaagt 40

<210> SEQ ID NO 38  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 38  
  
 tcttgtgtta ttcgcctgca ttgaaatccc atcccaatcc 40

<210> SEQ ID NO 39  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 39  
  
 tgagtgatct ctttgetgat cataaacata ttctccatc 40

<210> SEQ ID NO 40  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 40  
  
 tgcattcatt actaaataca cagggcatag cacatagtaa 40

<210> SEQ ID NO 41  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 41  
  
 cttcaatggt gccaggaaaa tccttgcagg aatcacaccc 40

<210> SEQ ID NO 42

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<211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 42  
  
 atttttttct aaagcttttag gaaatacaca cgtttcccct 40  
  
  
 <210> SEQ ID NO 43  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 43  
  
 agagtaatct tcaacaatcc ttggtctaaa cacacacaag 40  
  
  
 <210> SEQ ID NO 44  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 44  
  
 cccagggacc cacgccaagc tcaccgcacc ttccacaaaa 40  
  
  
 <210> SEQ ID NO 45  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 45  
  
 agctcctgta ctgactggtg ggggtggag cacacagccc 40  
  
  
 <210> SEQ ID NO 46  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 46  
  
 tcacacaggg aaagtgaggc ttggtggttg atttgagcaa 40  
  
  
 <210> SEQ ID NO 47  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 47  
  
 ccttccaaca gccgtgtgag acaagaggtc ttatctcttt 40  
  
  
 <210> SEQ ID NO 48  
 <211> LENGTH: 40

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 48

acaaggggtca ctgagcacaat gccatgtggt gggcacagtg 40

<210> SEQ ID NO 49  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 49

gtctcctaag tctcattott ttcttaggat tcttcagatc 40

<210> SEQ ID NO 50  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 50

tccgcctaag taaacataa aattacttaa gctgcgtaaa 40

<210> SEQ ID NO 51  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 51

cattttgacc tgattatott tgtctataag tcttaagcca 40

<210> SEQ ID NO 52  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 52

ccggttcctc caccctcact gcccacaaca ctgaaagaag 40

<210> SEQ ID NO 53  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 53

acagtgtggt gaaagaatcc ataactcttt ctttccagcc 40

<210> SEQ ID NO 54  
<211> LENGTH: 40  
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 54

gaagtttcat ctttatcaaa atctccattc ccaggcggac 40

<210> SEQ ID NO 55  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 55

aagtcattt ttttaagctt tgcgcttcag ctccagaaca 40

<210> SEQ ID NO 56  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 56

tcttcggtt gaatacaaat aggaaaacaa tcagacccaa 40

<210> SEQ ID NO 57  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 57

tcctcggggc attctagaac cgtagcagac ctgcttacat 40

<210> SEQ ID NO 58  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 58

tccttatgtg ggaaaataaa gaggatagac agatttgatt 40

<210> SEQ ID NO 59  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 59

agctgcgagt ccctaacaga cttccaggac agctgaaaaa 40

<210> SEQ ID NO 60  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 60

aggacaaggg agagacgccc acccgctct gtcaggata 40

<210> SEQ ID NO 61  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 61

aatccatgag ggtgacatac acatccttac tgttccaca 40

<210> SEQ ID NO 62  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 62

acttccttcc ctgagatgcc catcctttga ttctgggatt 40

<210> SEQ ID NO 63  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 63

gctcccggat aaattaatta ccgtgaccct gagctgcttc 40

<210> SEQ ID NO 64  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 64

tagactaaga gaatctaatt tgtggcaaag atcttgagtg 40

<210> SEQ ID NO 65  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 65

tgaaggatga ctaagagctt ccctataaac cccatactgg 40

<210> SEQ ID NO 66  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 66

agccaggact atagagtttc agaaaaggga gaaaattcta 40

<210> SEQ ID NO 67  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 67

tgctgctaataa ttaagtttct ggcaagtcaa aataaatctc 40

<210> SEQ ID NO 68  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 68

cgaaaacccat caattaacta gaatgatcag gaaattgcgt 40

<210> SEQ ID NO 69  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 69

tttatttagt ccccagggtg tatgaagtgc tcttcaggc 40

<210> SEQ ID NO 70  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 70

ggtccttctt ggtaccgata tgccatatt ggctggacat 40

<210> SEQ ID NO 71  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 71

tggcttggtgta ggatgcactc acatgggctg tagtaatact 40

<210> SEQ ID NO 72  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 72

tatcaccagc ataacttgtg gttcttcagc cagtaatttc 40

<210> SEQ ID NO 73  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 73

gaacaactgg gtatctacag gcaaagaaat gaaccttgac 40

<210> SEQ ID NO 74  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 74

taggtactgt tgtgtcccta tatattgac ttggtaataa 40

<210> SEQ ID NO 75  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 75

tatgtgaaca tcggtgaata tcataattta ttatgcaaac 40

<210> SEQ ID NO 76  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 76

agctgaacac tctttgtggt cctcttgaag cctagaatta 40

<210> SEQ ID NO 77  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 77

ccccacctca ctgcccccca gttctgactc acggtgtccc 40

<210> SEQ ID NO 78  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

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&lt;400&gt; SEQUENCE: 78

actcccatca cctggccagc ttggtgtcc cctgaccac 40

&lt;210&gt; SEQ ID NO 79

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 79

ggctgcccag ctgccagca gcaaaactgc ataggaactc 40

&lt;210&gt; SEQ ID NO 80

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 80

gccaggacg ccaagtgtca ccaccctctc cccaggcagg 40

&lt;210&gt; SEQ ID NO 81

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 81

cacaaggtca gctccaccg tgggtcagtg tgccccagat 40

&lt;210&gt; SEQ ID NO 82

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 82

ggagacaaaa cgggcacca gccagtcac gcccgctcct 40

&lt;210&gt; SEQ ID NO 83

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 83

ctgaaatcag tcagcagttt cggtagtct gcagctgaca 40

&lt;210&gt; SEQ ID NO 84

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 84

cgccacattt ggggctggga gagatgtcac aggggctgac 40

<210> SEQ ID NO 85

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 85

cacatgttct ctgcataggt tttaagcag ccagcagctg 40

<210> SEQ ID NO 86

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 86

tttaaatga aaaccacac ttccaaaata gcacttgagt 40

<210> SEQ ID NO 87

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 87

aacatgtttg tgtaattaag cattttaaaa tcataacat 40

<210> SEQ ID NO 88

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 88

tgcttatctg tgctttttat gttccacccc cccaccacca 40

<210> SEQ ID NO 89

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 89

attaataata attctgtgtt tatggggatt gcagatacat 40

<210> SEQ ID NO 90

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 90

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ccagctttgt gtcttcatga cccaactgga gtaagaatgg 40

<210> SEQ ID NO 91  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 91

aaagacctca tttgcagcat ggtagcagt gtcaaacatt 40

<210> SEQ ID NO 92  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 92

tctcgtagca ctggctgcag ccggcctgtg tgtgcccacc 40

<210> SEQ ID NO 93  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 93

gccttcatcc tgaacggctg accagcggaa acaaaagatc 40

<210> SEQ ID NO 94  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 94

atggccagat aacagtgttt agacatgtct ttgatgtttt 40

<210> SEQ ID NO 95  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 95

ccctgactgt gtaaggggtc tctctccatg ggaatagag 40

<210> SEQ ID NO 96  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 96

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ctgagcttag cttctactgt gctgttaatt tcaggcaaga 40

<210> SEQ ID NO 97  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 97

agatcaataa tatttgcat agctacttac atcagtctct 40

<210> SEQ ID NO 98  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 98

taattgcaga aaactataa agcatggaag aatacaaac 40

<210> SEQ ID NO 99  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 99

aaacaaattc ctctacctgg acatgactgt tgtagcatt 40

<210> SEQ ID NO 100  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 100

gggagattct tcatactctt ttaatgtaga tatgcacatt 40

<210> SEQ ID NO 101  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 101

acaaaaagg ctatcatatt gtacataaa ctttgctgta 40

<210> SEQ ID NO 102  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 102

tctgctagga acctgtaccc atgtcattac tgtaagcatt 40

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<210> SEQ ID NO 103  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 103  
  
actactcaaa ttttagtatac tgcagatatac agatatacctt 40

<210> SEQ ID NO 104  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 104  
  
tgaaatggta ttgtgacct tctgattag taaagtatac 40

<210> SEQ ID NO 105  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 105  
  
ttataatcta gcaaggtag agatcatgga tcactttcag 40

<210> SEQ ID NO 106  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 106  
  
acagcttgcc tccgataagc cagaattcca gagcttctgg 40

<210> SEQ ID NO 107  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 107  
  
tcaatcaacc tgatagctta ggggataaac taatttgaag 40

<210> SEQ ID NO 108  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 108  
  
gatcatgaag gatgaaagaa tttaccaat attataataa 40

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<210> SEQ ID NO 109  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 109

ttagccatc tgtatcaatg agcagatata agctttacac 40

<210> SEQ ID NO 110  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 110

aggggtagat tatttatgct gcccatTTTT agaccataaa 40

<210> SEQ ID NO 111  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 111

cactaccatt tcacaattcg cactttcttt ctttgcctt 40

<210> SEQ ID NO 112  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 112

gctccatcaa atcataaagg acccacttca aatgccatca 40

<210> SEQ ID NO 113  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 113

tcctactttc aggaacttct ttctcctaac gtcttctgcc 40

<210> SEQ ID NO 114  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 114

aattctatTT tttcttcaac gtacttttagg cttgtaatgt 40

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<210> SEQ ID NO 115  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 115

taagatgcaa atagtaagcc tgagcccttc tgtctaactt 40

<210> SEQ ID NO 116  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 116

ctgtgtttca gaataaaata ccaactctac tactctcatc 40

<210> SEQ ID NO 117  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 117

gaaacatgt ttatctcagg ttacaaatc tccacttgtc 40

<210> SEQ ID NO 118  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 118

ctttggaaaa gtaatcaggt ttagaggagc tcatgagagc 40

<210> SEQ ID NO 119  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 119

gctgaatccc caactcccaa ttggtccat ttgtggggga 40

<210> SEQ ID NO 120  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 120

ggtgttatga acttaacgct tgtgtctcca gaaaattcac 40

<210> SEQ ID NO 121

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<211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 121  
  
 agttaatgca cgtaataag caagagtta gtttaatgtg 40

<210> SEQ ID NO 122  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 122  
  
 taattgagaa ggcagattca ctggagtct tatataattg 40

<210> SEQ ID NO 123  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 123  
  
 cacggtcaga tgaatatata gtgtgaagaa tttgtataac 40

<210> SEQ ID NO 124  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 124  
  
 cacaagtcag catcagcgtg tcatgtctca gcagcagaac 40

<210> SEQ ID NO 125  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 125  
  
 ggaggtgggg acttaggtga aggaaatgag ccagcagaag 40

<210> SEQ ID NO 126  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 126  
  
 gtcacagcat tcaaggagg agacctcatt gtaagcttct 40

<210> SEQ ID NO 127  
 <211> LENGTH: 40

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<212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 127  
  
 aaagaggtga aattaatccc atacccttaa gtctacagac 40  
  
 <210> SEQ ID NO 128  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 128  
  
 ctttactaag gaacttttca tttaagtgt tgacgcgatgc 40  
  
 <210> SEQ ID NO 129  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 129  
  
 cagggttttcc tttccacggt aactacaatg aagtgatcct 40  
  
 <210> SEQ ID NO 130  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 130  
  
 gctctacagg gaggttgagg tgtagagat cagagcagga 40  
  
 <210> SEQ ID NO 131  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 131  
  
 tactatttcc aacggcatct ggcttttctc agcccttggtg 40  
  
 <210> SEQ ID NO 132  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 132  
  
 aaggtttagg cagggatagc cattctattt tattaggggc 40  
  
 <210> SEQ ID NO 133  
 <211> LENGTH: 40  
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 133  
  
aggggctcaa cgaagaaaaa gtgttccaag ctttaggaag 40

<210> SEQ ID NO 134  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 134  
  
gggctgaacc cccttcctcg gattgcagca cagcagcgag 40

<210> SEQ ID NO 135  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 135  
  
ctgacgtcat aatctaccaa ggtcatggat cgagttcaga 40

<210> SEQ ID NO 136  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 136  
  
gaaggtagag ctctcctoca ataagccaga tttccagagt 40

<210> SEQ ID NO 137  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 137  
  
caccaatatt attataattc ctatcaacct gataggttag 40

<210> SEQ ID NO 138  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 138  
  
agatataagc cttacacagg attatgaagt ctgaaaggat 40

<210> SEQ ID NO 139  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 139

acatgtatct ttctggtctt ttagccgcct aacactttga 40

<210> SEQ ID NO 140  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 140

caaagaacaa gtgcaatatg tgcagctttg ttgctcaggt 40

<210> SEQ ID NO 141  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 141

tattattatg tgagtaactg gaagatactg ataagttgac 40

<210> SEQ ID NO 142  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 142

taaaaatctt tctcacccat ccttagattg agagaagtca 40

<210> SEQ ID NO 143  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 143

ttgggttcac ctgagctctc ataactctga ccagcatacc 40

<210> SEQ ID NO 144  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 144

cacacccatc tcacagatcc cctatcttaa agagacccta 40

<210> SEQ ID NO 145  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 145

atggaaccca accagactct cagatatggc caaagatcta 40

<210> SEQ ID NO 146  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 146

gacaccagtc tctgacacat tcttaaaggt caggctctac 40

<210> SEQ ID NO 147  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 147

agagattcaa aagattcact tgtttaggcc ttagcgggct 40

<210> SEQ ID NO 148  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 148

tccttagtct gaggaggagc aattaagatt cacttgttta 40

<210> SEQ ID NO 149  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 149

taaatgggga agttgttga aacaggagg gatcctagat 40

<210> SEQ ID NO 150  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 150

gggtttatag atgactttta gaacactgcc ttggtttttg 40

<210> SEQ ID NO 151  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 151

aactcttaaa agatattgcc tcaaaagcat aagaggaaat 40

<210> SEQ ID NO 152  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 152

aaatcgagga ataagacagt tatggataag gagaaatcaa 40

<210> SEQ ID NO 153  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 153

tcagttagga tttaatcaat gtcagaagca atgatatagg 40

<210> SEQ ID NO 154  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 154

cttgaaaaca cttgaaattg cttgtgtaaa gaaacagttt 40

<210> SEQ ID NO 155  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 155

ataatcttca gaggaaagtt ttattctctg acttatttaa 40

<210> SEQ ID NO 156  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 156

agattccttc tgtcattttg cctctgttcg aatactttct 40

<210> SEQ ID NO 157  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

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&lt;400&gt; SEQUENCE: 157

atttcagctt ctaaacttta ttggcaatg ccttcccatg 40

&lt;210&gt; SEQ ID NO 158

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 158

gcaggagttt gttttcttct gcttcagagc tttgaattta 40

&lt;210&gt; SEQ ID NO 159

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 159

acatatcaac ggcaactgggtt ctttatctaa ctctctggca 40

&lt;210&gt; SEQ ID NO 160

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 160

ttatgcttcc ctgaaacaat accacctgct attctccact 40

&lt;210&gt; SEQ ID NO 161

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 161

ttctcactcc ctaccactga ggacaagttt atgtccttag 40

&lt;210&gt; SEQ ID NO 162

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 162

ttagagatta tgtcattacc agagttaaaa ttctataatg 40

&lt;210&gt; SEQ ID NO 163

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 163

ggtcattctt agaatagtaa tccagccaat agtacaggtt 40

<210> SEQ ID NO 164

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 164

caggcaataa gggcttttta agcaaacag ttgtgataaa 40

<210> SEQ ID NO 165

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 165

atgatgggca ctgaaggta aaacttgagt ctgtcaactt 40

<210> SEQ ID NO 166

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 166

aactcataaa tatccattt tccgctgaaa tatagcttta 40

<210> SEQ ID NO 167

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 167

cctggtttct ttgacctttt gggaccttga gtaagtaaag 40

<210> SEQ ID NO 168

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 168

cttcatttat tttcatgatt aaaattctaa gaaattcttg 40

<210> SEQ ID NO 169

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 169

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tttttaatta aattgcattg cctaagtat ttatgaacta 40

<210> SEQ ID NO 170  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 170

catagaaata aaacaatact ctgaagtagt tcagaatgtg 40

<210> SEQ ID NO 171  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 171

caatttatat aaagagtaa ttcaaagtag actattttaa 40

<210> SEQ ID NO 172  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 172

agggtttga atcttatgtc tagaaatttt gaaaaacctc 40

<210> SEQ ID NO 173  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 173

tatatgctaa gattccacct ctagtctag aactgagaag 40

<210> SEQ ID NO 174  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 174

tgacttggtg atctttttta aattctgaaa caacagcaac 40

<210> SEQ ID NO 175  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 175

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agctaaggac ttttctctgc ctatgcatgc tatcttcagt 40

<210> SEQ ID NO 176  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 176

tgattattta gattgaaac tataacatag tatgtttcct 40

<210> SEQ ID NO 177  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 177

aaaaaatgtg tatttctctg gagaaggta aaactgagga 40

<210> SEQ ID NO 178  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 178

caagtgagca aggcttaaat ggaagaagca atgatctcgt 40

<210> SEQ ID NO 179  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 179

ccaccttcac taacgagatc atccatcatg aggaaatatg 40

<210> SEQ ID NO 180  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 180

accaggcccc ctctgttttg tgcactaag ggtgaggatg 40

<210> SEQ ID NO 181  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 181

atgatttttc cctccccgg gcttctttta gccatcaata 40

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<210> SEQ ID NO 182  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 182  
  
 tagccccaca ggagtttggt ctgaaagtaa acttccacaa 40

<210> SEQ ID NO 183  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 183  
  
 aagcttattg aggctaaggc atctgtgaag gaaagaaaca 40

<210> SEQ ID NO 184  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 184  
  
 ctctaaacca ctatgctgct agagcctctt ttctgtactc 40

<210> SEQ ID NO 185  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 185  
  
 ctcatcaga cactagtgtc accagttccc tcatatacct 40

<210> SEQ ID NO 186  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 186  
  
 tattttcttc ttcttgctgg tttagtcatg ttttctggga 40

<210> SEQ ID NO 187  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 187  
  
 ggcaaaccca ttattttttt cttagactt gggatggtga 40

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<210> SEQ ID NO 188  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 188

tgggcagcgt cagaaactgt gtgtggatat agataagagc 40

<210> SEQ ID NO 189  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 189

gactatgctg agctgtgatg agggaggggc ctagctaaag 40

<210> SEQ ID NO 190  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 190

tgagagtcag aatgctcctg ctattgctt ctcagtcgcc 40

<210> SEQ ID NO 191  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 191

ttggtttcta cacaagtaga tacatagaaa aggctatagg 40

<210> SEQ ID NO 192  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 192

tgtttgagag tcctgcatga ttagttgctc agaaatgccc 40

<210> SEQ ID NO 193  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 193

ttacaaatat gtgattatca tcaaaactgt agggctaaag 40

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<210> SEQ ID NO 194  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 194  
  
cagataactt gcaagtctcta ggataccagg aaaataaatt 40

<210> SEQ ID NO 195  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 195  
  
agcattatgt ctgtctgtca ttgttttca tctcttctgta 40

<210> SEQ ID NO 196  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 196  
  
ttcacagtta cccacacagg tgaacccttt tagctctcct 40

<210> SEQ ID NO 197  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 197  
  
gaatgtttct ttctctctcag gatcagagtt gectacatct 40

<210> SEQ ID NO 198  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 198  
  
aatgcaccaa gactggcctg agatgtatcc ttaagatgag 40

<210> SEQ ID NO 199  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 199  
  
tcccagtagc accccaagtc agatctgacc ccgtagtgga 40

<210> SEQ ID NO 200

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<211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 200  
  
 gtgtcctcta acagcacagg ccttttgcca cctagtgtc 40

<210> SEQ ID NO 201  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 201  
  
 ggcaacaag gtttgtttc ttttctggtt ttcatgcctt 40

<210> SEQ ID NO 202  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 202  
  
 ttccatatcc ttgtttcata ttaatacatg tgtatagatc 40

<210> SEQ ID NO 203  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 203  
  
 aaatctatac acatgtatta ataaagcctg attctgccgc 40

<210> SEQ ID NO 204  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 204  
  
 aggtatagag gccacctgca agataaatat ttgattcaca 40

<210> SEQ ID NO 205  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 205  
  
 ctaatcattc tatggcaatt gataacaaca aatatatata 40

<210> SEQ ID NO 206  
 <211> LENGTH: 40

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<212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 206  
 ataatatatt ctagaatattg tcacattctg tctcaggcat 40

<210> SEQ ID NO 207  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 207  
 tttctttatg atgccgtttg aggtggagtt ttagtcaggt 40

<210> SEQ ID NO 208  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 208  
 agcttctcct tttttttgcc atctgccttg taagcctcct 40

<210> SEQ ID NO 209  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 209  
 gggaccacaga taggagtcac cactctaggc tgagaacac 40

<210> SEQ ID NO 210  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 210  
 cacacaccct aagcctcagc atgactcacc atgactcagc 40

<210> SEQ ID NO 211  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 211  
 ctgtgcttga gccagaaggt ttgcttagaa ggttacacag 40

<210> SEQ ID NO 212  
 <211> LENGTH: 40  
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 212  
  
 aactgctcat gcttggaacta tggagggtca ctaatggaga 40  
  
 <210> SEQ ID NO 213  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 213  
  
 cagaaatgta acaggaacta aggaaaaact gaagcttatt 40  
  
 <210> SEQ ID NO 214  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 214  
  
 cagagatgag gatgctggaa gggatagagg gagctgagct 40  
  
 <210> SEQ ID NO 215  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 215  
  
 aaaagtatag taatcattca gcaaatggtt ttgaagcacc 40  
  
 <210> SEQ ID NO 216  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 216  
  
 gtatcttatt cccacaaga gtccaagtaa aaaataacag 40  
  
 <210> SEQ ID NO 217  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 217  
  
 gaaaagaatg tttctctcac tgtggattat ttagagagt 40  
  
 <210> SEQ ID NO 218  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 218

aatggtcaag atttttttaa aaattaagaa aacataagtt 40

<210> SEQ ID NO 219  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 219

cttgagaaat gaaaatttat ttttttggtg gaggataccc 40

<210> SEQ ID NO 220  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 220

tctatctccc atcagggcaa gctgtaagga actggctaag 40

<210> SEQ ID NO 221  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 221

agtgagacag agtgacttag tcttagaggc cccactggta 40

<210> SEQ ID NO 222  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 222

gatgagaagg caccttcac actcatcaca gtcagctctg 40

<210> SEQ ID NO 223  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 223

tctctctct ctttctcat cagaaatttc ataagtctac 40

<210> SEQ ID NO 224  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 224

gtcaggcaga tcacataaga aaaggatg ccagttaagg 40

<210> SEQ ID NO 225  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 225

gttgctgtta gacaatttca tctgtgcct gcttaggagc 40

<210> SEQ ID NO 226  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 226

tctttaatga aagctaagct ttcattaaaa aaagtctaac 40

<210> SEQ ID NO 227  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 227

tgcattcgac tttgactgca gcagctgggtt agaaggttct 40

<210> SEQ ID NO 228  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 228

gaggagggtc ccagcccatt gctaaattaa catcaggctc 40

<210> SEQ ID NO 229  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 229

actggcagta tatctctaac agtggttgat gctatcttct 40

<210> SEQ ID NO 230  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 230

cttgctgct acattgagac cactgacca tacataggaa 40

<210> SEQ ID NO 231  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 231

atagctctgt cctgaactgt taggccactg gtccagagag 40

<210> SEQ ID NO 232  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 232

catctccttt gatcctcata ataaccctat gagatagaca 40

<210> SEQ ID NO 233  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 233

tattactctt accttataga tgatgacct gaaaacatag 40

<210> SEQ ID NO 234  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 234

caaggcactt gccctagct gggggtatag gggagcagtc 40

<210> SEQ ID NO 235  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 235

gtagtagtag aatgaaaaat gctgctatgc tgtgctccc 40

<210> SEQ ID NO 236  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

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&lt;400&gt; SEQUENCE: 236

ctttcccatg tctgccctct actcatggtc tatctctctc 40

&lt;210&gt; SEQ ID NO 237

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 237

cctgggagtc atggactcca cccagcacca ccaacctgac 40

&lt;210&gt; SEQ ID NO 238

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 238

ccacctatct gagcctgcca gcctataacc catctgggcc 40

&lt;210&gt; SEQ ID NO 239

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 239

tagctggtgg ccagccctga cccccccca cctccctg 40

&lt;210&gt; SEQ ID NO 240

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 240

tctgatagac acatctggca caccagctcg caaagtcacc 40

&lt;210&gt; SEQ ID NO 241

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 241

gggtcttggtg tttgctgagt caaaattcct tgaatccaa 40

&lt;210&gt; SEQ ID NO 242

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 242

ttagagactc ctgctcccaa atttacagtc atagacttct 40

<210> SEQ ID NO 243

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 243

ggctgtctcc tttatccaca gaatgattcc ttgcttcat 40

<210> SEQ ID NO 244

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 244

ccatccatct gatctctctc atcagtgag cacagggccc 40

<210> SEQ ID NO 245

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 245

gcagtagctg cagagtctca cataggtctg gcactgcctc 40

<210> SEQ ID NO 246

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 246

atgtccgacc ttaggcaaat gcttgactct tctgagctca 40

<210> SEQ ID NO 247

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 247

tgatcaggca aataaagat aataatagtg tttttttatg 40

<210> SEQ ID NO 248

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 248

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tagcgtgagg atgaaaaaca atagcaaaat tgattagact 40

<210> SEQ ID NO 249  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 249

aaggtctcaa caaatagtag tagattttat cgtccattaa 40

<210> SEQ ID NO 250  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 250

tccctctcct ctcttactca tcccatcacg tatgcctctt 40

<210> SEQ ID NO 251  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 251

ttcccttacc tataataaga gttattctctc ttattatatt 40

<210> SEQ ID NO 252  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 252

ttatagtgat tctggatatt aaagtgggaa tgaggggcag 40

<210> SEQ ID NO 253  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 253

ctaacgaaga agatgtttct caaagaagcc attctcccga 40

<210> SEQ ID NO 254  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 254

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gatcatctca gcagggttca ggaagataaa ggaggatcaa 40

<210> SEQ ID NO 255  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 255

tgttgaggtg ggaggaccgc ttgagcctgg gaagtgaag 40

<210> SEQ ID NO 256  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 256

agtgagccga gattttgccca ctacactccc atttgggtga 40

<210> SEQ ID NO 257  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 257

gtgagaccct ttctcaaaaa caaactaatt aaaaaaccct 40

<210> SEQ ID NO 258  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 258

tttacagatg aagaaactga gtcatacaac tactaagaga 40

<210> SEQ ID NO 259  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 259

gagtcactaa tcactcaggt ggtctggctc cagcatctgt 40

<210> SEQ ID NO 260  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 260

ttaatctctg ctctatactg cccaagactt ttataaagtc 40

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<210> SEQ ID NO 261  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 261  
  
gttgagtcac tgaaatgagt tattgggatg gctgtgtggg 40

<210> SEQ ID NO 262  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 262  
  
gtgctaagtt ctttcctaaa ggtatgtgag aatacaaagg 40

<210> SEQ ID NO 263  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 263  
  
aagcatcctc ctttttacac acgtgaacta gtgcatgcaa 40

<210> SEQ ID NO 264  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 264  
  
gacactcagt gggcctgggt gaaggtgaga attttattgc 40

<210> SEQ ID NO 265  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 265  
  
tgagagcctc tggggacatc ttgccagtca atgagtctca 40

<210> SEQ ID NO 266  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 266  
  
caatttcctt ctcagtcttg gagtaacaga agctcatgca 40

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<210> SEQ ID NO 267  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 267

ataaacggaa atttgtatt gaaatgagag ccattgaaa 40

<210> SEQ ID NO 268  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 268

ttactccaga ctctactta taaaaagaga aactgaggct 40

<210> SEQ ID NO 269  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 269

gaaggggtggg gactttctca gtatgacatg gaaatgatca 40

<210> SEQ ID NO 270  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 270

tggattcaaa gctcctgact ttctgtctag tgtatgtgca 40

<210> SEQ ID NO 271  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 271

gcccttttc ctctaactga aagaaggaaa aaaaaatgga 40

<210> SEQ ID NO 272  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 272

aaaatattct acatagtttc catgtcacag ccagggtgg 40

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<210> SEQ ID NO 273  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 273  
  
 tctcctgtta tttcttttaa aataaatata tcatttaaat 40

<210> SEQ ID NO 274  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 274  
  
 aaataagcaa accctgctcg ggaatgggag ggagagtctc 40

<210> SEQ ID NO 275  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 275  
  
 gtccaccct tctcggcct ggctctgcag atagtctat 40

<210> SEQ ID NO 276  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 276  
  
 gccctgacag agcctgccc attgctgggc cttggagtga 40

<210> SEQ ID NO 277  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 277  
  
 gcctagtaga gaggcagggc aagccatctc atagctctg 40

<210> SEQ ID NO 278  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 278  
  
 ggagagagaa aagggtcat tgtctataaa ctcaggctcat 40

<210> SEQ ID NO 279

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<211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 279  
  
 attcttattc tcacactaag aaaaagaatg agatgtctac 40

<210> SEQ ID NO 280  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 280  
  
 accctgcgtc ccctcttctg tactggggtc cccaagagct 40

<210> SEQ ID NO 281  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 281  
  
 aaaagtgatg gcaaagtc at tgcgctagat gccatcccat 40

<210> SEQ ID NO 282  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 282  
  
 tataaacctg catttgtctc cacacaccag tcatggacaa 40

<210> SEQ ID NO 283  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 283  
  
 cctctccca ggtccacgtg cttgtctttg tataatactc 40

<210> SEQ ID NO 284  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 284  
  
 aatttcggaa aatgtattct tcaatcttg ttctgttatt 40

<210> SEQ ID NO 285  
 <211> LENGTH: 40

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<212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 285  
  
 ttccaatggc ttagtagaaa aagtacatac ttgttttccc 40  
  
 <210> SEQ ID NO 286  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 286  
  
 attgacaata gacaatttca catcaatgtc tatatggggtc 40  
  
 <210> SEQ ID NO 287  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 287  
  
 tgtttgetgt gtttgcaaaa actcacaata actttatatt 40  
  
 <210> SEQ ID NO 288  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 288  
  
 ctactctaag aaagttacaa catggtgaat acaagagaaa 40  
  
 <210> SEQ ID NO 289  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 289  
  
 ttacaagtcc agaaaataaa agttatcatc ttgaggcctc 40  
  
 <210> SEQ ID NO 290  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 290  
  
 ttctaggaat aatatcaata ttacaaaatt aatctaacaa 40  
  
 <210> SEQ ID NO 291  
 <211> LENGTH: 40  
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 291  
  
 gaacagcaat gagataatgt gtacaaagta cccagaccta 40  
  
 <210> SEQ ID NO 292  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 292  
  
 gtagagcatc aaggaagcgc attgcggagc agttttttgt 40  
  
 <210> SEQ ID NO 293  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 293  
  
 ttgtttttgt attctgtttc gtgaggcaag gtttcactct 40  
  
 <210> SEQ ID NO 294  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 294  
  
 tccaggctgg agtgcagtgg caagatcatg tctcactgca 40  
  
 <210> SEQ ID NO 295  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 295  
  
 tgacctcctg agctcaaggg atcctcccat ttcggcctcc 40  
  
 <210> SEQ ID NO 296  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 296  
  
 tagctgggac tacaggtgta catcacatgc ctggctaatt 40  
  
 <210> SEQ ID NO 297  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
probe

<400> SEQUENCE: 297

ttttttttt aagtagagac gaggtcttgc tatgtgtgcc                40

<210> SEQ ID NO 298
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
probe

<400> SEQUENCE: 298

taatatcaaa ctcttgagct caagcagtcc tcccacttct                40

<210> SEQ ID NO 299
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
probe

<400> SEQUENCE: 299

tggaggatc cagtatgaaa ttagataat acctgccttc                40

<210> SEQ ID NO 300
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
probe

<400> SEQUENCE: 300

gttgaatta gaacttaatg atataatgca tcaatgaact                40

<210> SEQ ID NO 301
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
probe

<400> SEQUENCE: 301

atagttccta gcacaaagta agaatccttt caatgtgtgt                40

<210> SEQ ID NO 302
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
probe

<400> SEQUENCE: 302

gtgtatgtat ttatctgtta ttaataggaa tcttatgggc                40

<210> SEQ ID NO 303
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 303

tctcacttaa tccttattaa taactatgaa gcaggtattt 40

<210> SEQ ID NO 304  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 304

gagttttcca agtgagttaa gtagcttg taataactaa 40

<210> SEQ ID NO 305  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 305

atatccacag gttacatagc tagtatataa ctgagaaata 40

<210> SEQ ID NO 306  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 306

tatttatatt ataaaacatt ctaacaatac agatgtatat 40

<210> SEQ ID NO 307  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 307

taaaaaactg aaagggtca tgcaacccta ccttctcaat 40

<210> SEQ ID NO 308  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 308

cttcttctact tagaaaaaac cagccttagc tgtctgctat 40

<210> SEQ ID NO 309  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 309

cctttcaaaa tatacttctg agaaatgaga gagagaaatg 40

<210> SEQ ID NO 310  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 310

gggtagaagg aaggaagata gggtaagaga caggaagga 40

<210> SEQ ID NO 311  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 311

tggggaaaga aattaaatta ttcttttctc tgtctcttga 40

<210> SEQ ID NO 312  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 312

gctctttcca ttacattgaa tcaaaggtaa tgttgccatt 40

<210> SEQ ID NO 313  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 313

gactcttgaa ataaagaaag accgatgtat gaaataattt 40

<210> SEQ ID NO 314  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 314

agtctatggc attttcaaaa tgcaaggatga tgtcttacta 40

<210> SEQ ID NO 315  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

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&lt;400&gt; SEQUENCE: 315

gcctttgctt tattattaga aatggggaag tgagtataga 40

&lt;210&gt; SEQ ID NO 316

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 316

ttatcaggag atatattagg aaaaaggga actggagaaa 40

&lt;210&gt; SEQ ID NO 317

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 317

gaggagtatc cagatgtcct gtcctgtaa ggtgggggca 40

&lt;210&gt; SEQ ID NO 318

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 318

ccttcaatca aaagggtcc ttaacaactt ccttgcttgg 40

&lt;210&gt; SEQ ID NO 319

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 319

ccaccatctt ggaccattag ctccacaggt atcttcttcc 40

&lt;210&gt; SEQ ID NO 320

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 320

agtggtcata acagcagctt cagctacctc tctaagagt 40

&lt;210&gt; SEQ ID NO 321

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 321

ccagatatag gtcaggaaat ataatccact aataaaaaga 40

<210> SEQ ID NO 322

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 322

cattttgact gtagttgttt gttttttgtc attgtgacta 40

<210> SEQ ID NO 323

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 323

taacattctc actctttcat cagtaatcac tcaggttatt 40

<210> SEQ ID NO 324

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 324

gaccaacaga ctgtgggaaa aatcagagaa ggaggcatcc 40

<210> SEQ ID NO 325

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 325

gcttactagc ctaaactgaa attgctatag cagagtgaac 40

<210> SEQ ID NO 326

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 326

aggtttacag atattttoca caaagagtaa aaggattgaa 40

<210> SEQ ID NO 327

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 327

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tctccagatc aatgcatagg aaataataat ggaccataaa 40

<210> SEQ ID NO 328  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 328

atattatgac gaacaacatt aggataagtc catatcaatt 40

<210> SEQ ID NO 329  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 329

atccagtcac aagcacagac tacgtgaagc acgtccaagt 40

<210> SEQ ID NO 330  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 330

gcaggagaaa tgagaggagc aagaaagagg agccatttga 40

<210> SEQ ID NO 331  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 331

gaatagcaga aaaaggaaag gcaagtcata ttaacaaatg 40

<210> SEQ ID NO 332  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 332

tcatgccaac agtacagata actctgctaa taaagtaga 40

<210> SEQ ID NO 333  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 333

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taatacaggt agtagcagat atctacatag tagttaaagg 40

<210> SEQ ID NO 334  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 334

ggccatcagt acagaagatt ccataaagga gaacctaaag 40

<210> SEQ ID NO 335  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 335

agaataattt gtcagaagct taaaagctga actctgaggc 40

<210> SEQ ID NO 336  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 336

aactacaata tccttttgac tgtggaaagg gtggtgaaag 40

<210> SEQ ID NO 337  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 337

gttcaaggac atttgagcca acatagagag gaacattggc 40

<210> SEQ ID NO 338  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 338

tgagggatat ctgtcctgat gttgtccagg atggtgatga 40

<210> SEQ ID NO 339  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 339

catataaata acgtagagaa aacaggagg gatagagatc 40

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<210> SEQ ID NO 340  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 340  
  
caaagaggca tcaaagatag ggatgtttgt aaggatgaaa 40

<210> SEQ ID NO 341  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 341  
  
ctgttcttct ctgagtagcc aagctcagct tggttcaagc 40

<210> SEQ ID NO 342  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 342  
  
catactgtgg atctgtagca aattccccct gaaaaccag 40

<210> SEQ ID NO 343  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 343  
  
tctgaccctc acattcaagt tctgaggaag ggccaactgcc 40

<210> SEQ ID NO 344  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 344  
  
gccttgagat acctggtcct tattccttgg actttggcaa 40

<210> SEQ ID NO 345  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 345  
  
atagggcttg ttttagggag aaacctgttc tccaaactct 40

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<210> SEQ ID NO 346  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 346  
  
 ctggtgtcca tactctgaat ggaagaatg atgggattac 40

<210> SEQ ID NO 347  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 347  
  
 agcaggagag gatcaacccc atactctgaa tctaagagaa 40

<210> SEQ ID NO 348  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 348  
  
 tcagatccct ggatgcaagc caggtctgga accataggca 40

<210> SEQ ID NO 349  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 349  
  
 ctctcccta ccaccttag ccataaggaa acatggaatg 40

<210> SEQ ID NO 350  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 350  
  
 gacacaaacc tgggcctttc aatgctataa cctttcttga 40

<210> SEQ ID NO 351  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 351  
  
 ctacctgact tctgagtcag gatttataag ccttggtact 40

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<210> SEQ ID NO 352  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 352  
  
tgaaccaaca agcatcgaag caataatgag actgcccga 40

<210> SEQ ID NO 353  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 353  
  
gaaaagcaat aatccatddd tcatggatc tcatatgata 40

<210> SEQ ID NO 354  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 354  
  
taacacttat ctctctgaac tttgggcttt taatatagga 40

<210> SEQ ID NO 355  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 355  
  
ttttctgact gtetaatctt tctgatctat cctggatggc 40

<210> SEQ ID NO 356  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 356  
  
atcttcatcg aatttgggtg tttctttcta aaagtccttt 40

<210> SEQ ID NO 357  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 357  
  
gaaattacaa atgctaaagc aaacccaaac aggcaggaat 40

<210> SEQ ID NO 358

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<211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 358  
  
 attaggcatc ttacagtttt tagaatcctg catagaactt 40

<210> SEQ ID NO 359  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 359  
  
 tacaatattt gactcttcag gttaaacata tgtcataaat 40

<210> SEQ ID NO 360  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 360  
  
 aacattcagt gaagtgaagg gcctacttta cttaacaaga 40

<210> SEQ ID NO 361  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 361  
  
 tcttttccta tcagtggttt acaagccttg tttatatttt 40

<210> SEQ ID NO 362  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 362  
  
 tatttttggt ctgagaatat agatttagat acataatgga 40

<210> SEQ ID NO 363  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 363  
  
 caaaatctaa cacaaaatct agtagaatca tttgettaca 40

<210> SEQ ID NO 364  
 <211> LENGTH: 40

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<212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 364  
 agaatttatg acttgatgata tccaagtcac tctctggataa 40  
  
 <210> SEQ ID NO 365  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 365  
 ttacactaga aaatagccac aggcttctctg caaggcagcc 40  
  
 <210> SEQ ID NO 366  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 366  
 agtttgaaca cttgttatgg tctattctct cattctttac 40  
  
 <210> SEQ ID NO 367  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 367  
 acttcgtgag agatgaggca gaggtacact acgaaagcaa 40  
  
 <210> SEQ ID NO 368  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 368  
 tcttgagaat gagcctcagc cctggctcaa actcacctgc 40  
  
 <210> SEQ ID NO 369  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 369  
 aataggatgt ctgtgctcca agttgccaga gagagagatt 40  
  
 <210> SEQ ID NO 370  
 <211> LENGTH: 40  
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 370  
  
 attaaagatc cctcctgctt aattaacatt cacaagtaac 40  
  
  
 <210> SEQ ID NO 371  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 371  
  
 acttaaagta gcgataccct ttcaccctgt cctaatacaca 40  
  
  
 <210> SEQ ID NO 372  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 372  
  
 tctcaggtgt taactttata gtgaggactt tcttgccata 40  
  
  
 <210> SEQ ID NO 373  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 373  
  
 atagtttcat ataaatgggt tctcatcat ctatgggtac 40  
  
  
 <210> SEQ ID NO 374  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 374  
  
 ggtatttaca tttgccattc cctatgccct aaatatttaa 40  
  
  
 <210> SEQ ID NO 375  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 375  
  
 tattgatatt ccttgaaaat tctaagcatc ttacatcttt 40  
  
  
 <210> SEQ ID NO 376  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 376  
  
 cttttattct ccccttcacc gaatctcatc ctacattggc 40  
  
 <210> SEQ ID NO 377  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 377  
  
 tagtgtecca aattttataa ttaggactt ctatgatctc 40  
  
 <210> SEQ ID NO 378  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 378  
  
 atatggtcac ctctttgttc aaagtcttct gatagtttcc 40  
  
 <210> SEQ ID NO 379  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 379  
  
 acaatcttcc tgcttctacc actgccccac tacaatttct 40  
  
 <210> SEQ ID NO 380  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 380  
  
 agtcactgtc accaccacct aaattatagc tgttgactca 40  
  
 <210> SEQ ID NO 381  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 381  
  
 ctgaccctt gccttcacct ccaatgtac cactctggtc 40  
  
 <210> SEQ ID NO 382  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 382

agaaaatcct gttggttttt cgtgaaagga tgttttcaga 40

<210> SEQ ID NO 383  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 383

acataactc acagccagaa attagcatgc actagagtgt 40

<210> SEQ ID NO 384  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 384

acccaaagac tcactttgcc tagcttcaaa atccttactc 40

<210> SEQ ID NO 385  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 385

tgaggtagag actgtgatga acaaacacct tgacaaaatt 40

<210> SEQ ID NO 386  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 386

tccatatcca cccaccagc tttccaattt taaagccaat 40

<210> SEQ ID NO 387  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 387

aaggtatgat gtgtagacaa gctccagaga tggtttctca 40

<210> SEQ ID NO 388  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 388

ctctggtcag catccaagaa atacttgatg tcactttggc 40

<210> SEQ ID NO 389  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 389

aactgtgaac ttccttcagc tagaggggcc tggctcagaa 40

<210> SEQ ID NO 390  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 390

tgattgttct ctgacttatac taccattttc cctccttaaa 40

<210> SEQ ID NO 391  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 391

aaacaaaacc catcaaattc cctgaccgaa cagaattctg 40

<210> SEQ ID NO 392  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 392

cagaggtcac agcctaaaca tcaaattcct tgagggtcgg 40

<210> SEQ ID NO 393  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 393

gaaggcaggt gtggctctgc agtgtgattg ggtacttgca 40

<210> SEQ ID NO 394  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

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<400> SEQUENCE: 394  
catggaggaa aaactcatca gggatggagg cacgcctcta 40

<210> SEQ ID NO 395  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 395  
agcttgtaa attgaattct atccttctta ttcaattcta 40

<210> SEQ ID NO 396  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 396  
catagttgtc agcacaatgc ctaggctata ggaagtactc 40

<210> SEQ ID NO 397  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 397  
gcagatatag cttgatggcc ccatgcttgg ttaaacatcc 40

<210> SEQ ID NO 398  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 398  
ctaaataact agaatactct ttattttttc gtatcatgaa 40

<210> SEQ ID NO 399  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 399  
agtgtttaa gggatgatc agactaaact tgaaatatgt 40

<210> SEQ ID NO 400  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

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<400> SEQUENCE: 400

ggatgggtct agaagacta gcattgtttt aggttgagtg 40

<210> SEQ ID NO 401

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 401

tgctgccaac attaacagtc aagaaatacc tccgaataac 40

<210> SEQ ID NO 402

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 402

tattgtgaga ggtctgaata gtgttgtaaa ataagctgaa 40

<210> SEQ ID NO 403

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 403

ttacaacatg atggcttggt gtctaaatat ctctagggga 40

<210> SEQ ID NO 404

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 404

ctaagtagaa gggctactttc acaggaacag agagcaaaag 40

<210> SEQ ID NO 405

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 405

gtcttgatt gcccagtgac atgcacactg gtcaaaagta 40

<210> SEQ ID NO 406

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 406

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ccctatgtct tcctgatgg gctagagttc ctctttctca 40

<210> SEQ ID NO 407  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 407

aaagtttccc caaattttac caatgcaagc catttctcca 40

<210> SEQ ID NO 408  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 408

aactgcagat tctctgcatc tcctttgcc ggtctgaca 40

<210> SEQ ID NO 409  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 409

tagtgctgtg gtgctgtgat aggtacacaa gaaatgagaa 40

<210> SEQ ID NO 410  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 410

taactagcgt caagaactga gggccctaaa ctatgctagg 40

<210> SEQ ID NO 411  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 411

cattggctcc gtcttcatcc tgcagtgacc tcagtgcctc 40

<210> SEQ ID NO 412  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 412

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tgtttatgtg ttatagtgtt catttactct tctggtctaa 40  
  
 <210> SEQ ID NO 413  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 413  
  
 cctttgaccc cttggtcaag ctgcaacttt ggttaaaggg 40  
  
 <210> SEQ ID NO 414  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 414  
  
 ttctcttggg ttacagagat tgcatatga caaattataa 40  
  
 <210> SEQ ID NO 415  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 415  
  
 tggaagtgt ggtccaagcc acagttgcag accatacttc 40  
  
 <210> SEQ ID NO 416  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 416  
  
 ctgcctgtg gcccttgctt cttactttta cttcttgcg 40  
  
 <210> SEQ ID NO 417  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 417  
  
 aactcagata ttgtggatgc gagaaattag aagtagatat 40  
  
 <210> SEQ ID NO 418  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 418  
  
 tacagaacca ccaagtagta aggctaggat gtagaccag 40

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<210> SEQ ID NO 419  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 419  
  
tgagctctcc tactgtctac attacatgag ctcttattaa 40

<210> SEQ ID NO 420  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 420  
  
aagctaataa gtagacaatt agtaattaga agtcagatgg 40

<210> SEQ ID NO 421  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 421  
  
agcccaatgt acttgtagtg tagatcaact tattgaaagc 40

<210> SEQ ID NO 422  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 422  
  
ccaataactca gaagtagatt attacctcat ttattgatga 40

<210> SEQ ID NO 423  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 423  
  
gctagaatca aatttaagtt tatcatatga ggccgggcac 40

<210> SEQ ID NO 424  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 424  
  
taataactaat gataagtaac acctcttgag tacttagtat 40

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<210> SEQ ID NO 425  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 425

atggtaatc tgtgagatat gtattattga acatactata 40

<210> SEQ ID NO 426  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 426

tgaaagagaa gtgggaatta atacttactg aaatctttct 40

<210> SEQ ID NO 427  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 427

gagagacacg aggaatagt gtagatttag gctggaggta 40

<210> SEQ ID NO 428  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 428

gttgagaggg aaacaagatg gtgaaggac tagaaaccac 40

<210> SEQ ID NO 429  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 429

caaggttctg aacatgagaa attttttagga atctgcacag 40

<210> SEQ ID NO 430  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 430

tgccatctaa aaaaatctga cttcactgga aacatggaag 40

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<210> SEQ ID NO 431  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 431

gggatcctct cttaagtgtt tctgctgga atctctcac 40

<210> SEQ ID NO 432  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 432

gttcccttca tgtgacaggg agcctcctgc cccgaacttc 40

<210> SEQ ID NO 433  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 433

ttggataaga gtaggaaga acctagagcc tacgctgagc 40

<210> SEQ ID NO 434  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 434

atctggggct tgtgaagac tggcttaaaa tcagaagccc 40

<210> SEQ ID NO 435  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 435

accgcaatgc ttctgcca ttcagggtc cagcatgtag 40

<210> SEQ ID NO 436  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 436

tatggggaag cagggtatga aagagctctg aatgaaatgg 40

<210> SEQ ID NO 437

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<211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 437  
  
 ggttgcatga atcagattat caacagaaat gttgagacaa 40

<210> SEQ ID NO 438  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 438  
  
 aatgcaggcc taggcatgac tgaaggctct ctcataattc 40

<210> SEQ ID NO 439  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 439  
  
 taacgttttc ttgtctgcta ccccatcata tgcacaacaa 40

<210> SEQ ID NO 440  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 440  
  
 ttaattccca aactcatata gctctgagaa agtctatgct 40

<210> SEQ ID NO 441  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 441  
  
 ccctataggg gatttctacc ctgagcaaaa ggctggtctt 40

<210> SEQ ID NO 442  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 442  
  
 tcctcacat atagaaagct ttaacccat cattgaataa 40

<210> SEQ ID NO 443  
 <211> LENGTH: 40

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 443

taagctgtct agcaaaagca agggcttgga aaatctgtga 40

<210> SEQ ID NO 444  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 444

aggattagaa gattcttctg tgtgtaagaa tttcataaac 40

<210> SEQ ID NO 445  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 445

attatcttct ggaatagga atcaagttat attatgtaac 40

<210> SEQ ID NO 446  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 446

ctctctgggt gactgtaga gttctggcac ttgtcactat 40

<210> SEQ ID NO 447  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 447

tcttcagtta gatggtaac tttgtgaagt tgaaaactgt 40

<210> SEQ ID NO 448  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 448

ctacaccatg tggagaaggg gtggtggttt tgattgctgc 40

<210> SEQ ID NO 449  
<211> LENGTH: 40  
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 449  
  
 actttcctaa cctgagccta acatccctga catcaggaaa 40  
  
 <210> SEQ ID NO 450  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 450  
  
 tacactttat tcgtctgtgt cctgctctgg gatgatagtc 40  
  
 <210> SEQ ID NO 451  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 451  
  
 tactctttgc attccactgt ttttcctaag tgactaaaaa 40  
  
 <210> SEQ ID NO 452  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 452  
  
 aaaggcctcc caggccaagt tatccattca gaaagcattt 40  
  
 <210> SEQ ID NO 453  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 453  
  
 tattgacatg tacttcttgg cagtctgtat gctggatgct 40  
  
 <210> SEQ ID NO 454  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 454  
  
 tttggtccta attatgtctt tgctcactat ccaataaata 40  
  
 <210> SEQ ID NO 455  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 455

gttaaaaaaa ctacctctca acttgctcaa gcatacactc 40

<210> SEQ ID NO 456  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 456

taattagtgc ttgcataat taatcatatt taatactctt 40

<210> SEQ ID NO 457  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 457

actagtgttc tgtactttat gccattcat cttaactgt 40

<210> SEQ ID NO 458  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 458

gtattttttg ttaactgca atcattcttg ctgcagggtga 40

<210> SEQ ID NO 459  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 459

gcagtgactt ataaatgcta actactctag aaatgtttgc 40

<210> SEQ ID NO 460  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 460

ttataagcat gattacagga gttttaacag gctcataaga 40

<210> SEQ ID NO 461  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 461

agtatccctc aagtagtgtc aggaattagt catttaaata 40

<210> SEQ ID NO 462  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 462

agtcacccat ttgtatatt aaagatgtgt tgtctactgt 40

<210> SEQ ID NO 463  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 463

tggtcataaa acattgaatt ctaatctccc tctcaaccct 40

<210> SEQ ID NO 464  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 464

acagttgaaa agacctaagc ttgtgcctga tttaagcett 40

<210> SEQ ID NO 465  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 465

caactacagg gccttgaact gcacactttc agtccggctc 40

<210> SEQ ID NO 466  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 466

gtggttcttt gaagagactt ccacctggga acagttaaac 40

<210> SEQ ID NO 467  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 467

tggaggaaat atttatcccc aggtagttcc ctttttgcac 40

<210> SEQ ID NO 468  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 468

gcctggtgct tttggtaggg gagcttgcac tttccccctt 40

<210> SEQ ID NO 469  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 469

tctcatttct ttgagaactt cagggaaaat agacaaggac 40

<210> SEQ ID NO 470  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 470

caaaccttttc aagccttctc taatcttaaa ggtaaacaag 40

<210> SEQ ID NO 471  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 471

tcaacaaagg agaaaagttt gttggcctcc aaaggcacag 40

<210> SEQ ID NO 472  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 472

gatgcaacag accttgaag catacaggag agctgaactt 40

<210> SEQ ID NO 473  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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&lt;400&gt; SEQUENCE: 473

catctgagat cccagcttct aagaccttca attctcactc 40

&lt;210&gt; SEQ ID NO 474

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 474

tatcttaaca gtgagtgaac aggaaatctc ctcttttccc 40

&lt;210&gt; SEQ ID NO 475

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 475

aactcatgct ttgtagatga ctagatcaaa aaatttcagc 40

&lt;210&gt; SEQ ID NO 476

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 476

tcaaaggaag tcaaaagatg tgaaaaacaa tttctgacct 40

&lt;210&gt; SEQ ID NO 477

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 477

tgcttcact taagtaatca attcctaggt tatattctga 40

&lt;210&gt; SEQ ID NO 478

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 478

ccctaccttg ttcaaaatgt tcctgtccag accaaagtac 40

&lt;210&gt; SEQ ID NO 479

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 479

gcacttacaa attatactac gctctatact ttttgtttaa 40

<210> SEQ ID NO 480

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 480

ctttagtttc atttcaaaca atccatacac acacagccct 40

<210> SEQ ID NO 481

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 481

tagggaccac aggggtaagg gggcagtaga attatactcc 40

<210> SEQ ID NO 482

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 482

ctcacaatta agctaagcag ctaagagtct tgcagggtag 40

<210> SEQ ID NO 483

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 483

gttgaaagac agagaggatg gggtgctatg ccccaaatca 40

<210> SEQ ID NO 484

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 484

gcttgctctaa ttttatatat caccctactg aacatgacct 40

<210> SEQ ID NO 485

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 485

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aatattgtac acgtacacca aagcatcatg ttgtaccca 40

<210> SEQ ID NO 486  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 486

tgtgaagtgg tggatttggtt aattagcctt atttaacat 40

<210> SEQ ID NO 487  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 487

tgacacatat gacattttaa ctatgttcca gattttgaa 40

<210> SEQ ID NO 488  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 488

gcaaggaatc attcaatggt ttctaaatct attactgcat 40

<210> SEQ ID NO 489  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 489

cattttcata ggttttcttc gattgatcat tattcatgat 40

<210> SEQ ID NO 490  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 490

aaagtgatca agatattttt agttcaggct ccaaaatttt 40

<210> SEQ ID NO 491  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 491

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 ctttacaggc cgagaaaaat gaatctgaat tcctgacctc 40

<210> SEQ ID NO 492  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

&lt;400&gt; SEQUENCE: 492

tccactcaag gcctacattc tgctataatg caatttcaag 40

<210> SEQ ID NO 493  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

&lt;400&gt; SEQUENCE: 493

aactgcttaa aattaatggc acaagtcacg tttttgatgt 40

<210> SEQ ID NO 494  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

&lt;400&gt; SEQUENCE: 494

ctgactgtga cgtagcaata aagaaacca cgtttcatat 40

<210> SEQ ID NO 495  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

&lt;400&gt; SEQUENCE: 495

ctggcccact gcttgaggga gagcactcag gaccatgaac 40

<210> SEQ ID NO 496  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

&lt;400&gt; SEQUENCE: 496

ttctgaaatg ataaagtcaa tcacaggaag gcacctggac 40

<210> SEQ ID NO 497  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

&lt;400&gt; SEQUENCE: 497

atcattctct ttccttctct ctatgtggca gaaagtaaaa 40

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<210> SEQ ID NO 498  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 498  
  
ggagataata atgtgttact ccctaaggca gagtgcctt 40

<210> SEQ ID NO 499  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 499  
  
caattaactt ggccatgtga ctggttgtga ctaaaataat 40

<210> SEQ ID NO 500  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 500  
  
cactaaatca atatacttct caacaatttc caacagccct 40

<210> SEQ ID NO 501  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 501  
  
ctaggctcct gagtttgcg gggatgcgaa gaacccttat 40

<210> SEQ ID NO 502  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 502  
  
ccgaggacc cgcactcgga gccgccagcc ggccccaccg 40

<210> SEQ ID NO 503  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 503  
  
ttggaagcac aggtgtggg ataagtctaa ttactagtga 40

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<210> SEQ ID NO 504  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 504

gttcagtatg cctttgattt tacaataata ttctgttat 40

<210> SEQ ID NO 505  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 505

agattccatg aagtattaca gcatttggtg gtctttttgc 40

<210> SEQ ID NO 506  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 506

tatttgctct gaaataagac ataattggg gtgagaaagc 40

<210> SEQ ID NO 507  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 507

actcatgata tttggctcta gaatacatgc tctgaatcat 40

<210> SEQ ID NO 508  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 508

tccaagatga agtggctact aactgacaga gggcataatt 40

<210> SEQ ID NO 509  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 509

tattcacagt aactctgtgc ctcaagtact attgtaatac 40

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<210> SEQ ID NO 510  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 510  
  
acatcctcaa tctacacact aggatagtat aaaagtaata 40

<210> SEQ ID NO 511  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 511  
  
gtctacccat atgtgacctt catgtctttg ctctaagccc 40

<210> SEQ ID NO 512  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 512  
  
cgtgtaatcc ttgacaatgt catctcatct atttattccc 40

<210> SEQ ID NO 513  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 513  
  
tctgaaagag actaaccttc cctcgctttg cagagaaaga 40

<210> SEQ ID NO 514  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 514  
  
atgcatggat tctcttgaaa aaatgtttct gccatgatgt 40

<210> SEQ ID NO 515  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 515  
  
tagttgaaga cctactgtgt tcagggccgt gagccagggc 40

<210> SEQ ID NO 516

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<211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 516  
  
 caacgtggag agctgtcctg gcaccatttc ttcctgctgt 40

<210> SEQ ID NO 517  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 517  
  
 atcctcaaag gagcctggct tgggctaaca aggaagaact 40

<210> SEQ ID NO 518  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 518  
  
 tgccctgggac cctgccccaa gcaaagtaat aatctgaatg 40

<210> SEQ ID NO 519  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 519  
  
 ctggtgtgtc cagtgtgatc cctgcacca tgcccggagc 40

<210> SEQ ID NO 520  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 520  
  
 ctgccccctg cagcagggaa ggggctctgg aagggtctga 40

<210> SEQ ID NO 521  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 521  
  
 tagctgtgtc cccactatgc accatcgctt atctgttett 40

<210> SEQ ID NO 522  
 <211> LENGTH: 40

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 522

gaaaccgaa aaatgtctctg gtctcttct taagtctggg 40

<210> SEQ ID NO 523  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 523

gctgagaaca tgactctgct tggcgttcca ttaattgac 40

<210> SEQ ID NO 524  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 524

gagagggtgt gcatttgaag tatagatttg ttaaacaatag 40

<210> SEQ ID NO 525  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 525

catcaggcaa aaatacttcg atgggactgt gttctttcag 40

<210> SEQ ID NO 526  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 526

tctaaagtga tgtaatgttg ccacggaat tctaaccct 40

<210> SEQ ID NO 527  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 527

cgtgcagaac cagctctgtc ttcccagaca ctgctgcttt 40

<210> SEQ ID NO 528  
<211> LENGTH: 40  
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 528  
  
 acccctgagc acctcagtgt ccgtgactgt ggagcggagg 40

<210> SEQ ID NO 529  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 529  
  
 ctgcctggga cacgtaaggc tgcccagtga tctgagcgc 40

<210> SEQ ID NO 530  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 530  
  
 cacagccgga tgggtgagg gctggcactg ccggggctcc 40

<210> SEQ ID NO 531  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 531  
  
 cgtcttgga gaggctccct gtcataagg acctgaggtt 40

<210> SEQ ID NO 532  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 532  
  
 gaccccaaa agatgagcgg gtccccttcc caattttcgg 40

<210> SEQ ID NO 533  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 533  
  
 tcaggaagcc ggtgctcagc aaacttatct gaagctcttg 40

<210> SEQ ID NO 534  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 534

gaggctgcag aggaacatcg tttggtcaaa tgtgaaatgt 40

<210> SEQ ID NO 535  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 535

ctagcttcta gaaagtgctg ccaatttggg gaccaaggga 40

<210> SEQ ID NO 536  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 536

ggaaacactt ctttttcct tgacaaagga catcctctgc 40

<210> SEQ ID NO 537  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 537

gcatgtgcat aaacactcgt gtgtgtgtcc ttttatccca 40

<210> SEQ ID NO 538  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 538

ccaaactctc atacatgtcc atagagagag gcagacgtat 40

<210> SEQ ID NO 539  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 539

gggttgaaga caaggggctc agagcttgct ttttatacac 40

<210> SEQ ID NO 540  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 540

agattcatct tcatggcagg acttcaggca agagaggccc 40

<210> SEQ ID NO 541  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 541

ctcaccctt agcaggacc tgacggaact ggttacaggc 40

<210> SEQ ID NO 542  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 542

ggttgggaga caatgggtgg ccctcggtg tgggtcctc 40

<210> SEQ ID NO 543  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 543

agagtctaga gggcccgtgg ggacgggagt cctgggaacc 40

<210> SEQ ID NO 544  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 544

gcgcatgtc cggcttcacc ctgccagaa tcacagcctc 40

<210> SEQ ID NO 545  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 545

atggttaaaa aattctccta cttaagactc ccagaccctc 40

<210> SEQ ID NO 546  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 546

ggggtgaaga caaggggctc agagcttgct tttatacac 40

<210> SEQ ID NO 547  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 547

agattcatct tcattggcagg acttcaggca agagaggccc 40

<210> SEQ ID NO 548  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 548

ctcaccctt agcaggacc tgacggaact ggttacaggc 40

<210> SEQ ID NO 549  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 549

ggttgggaga caatgggtgg cccctcggtg tgggtcctc 40

<210> SEQ ID NO 550  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 550

agagtctaga gggcccgtgg ggacgggagt cctgggaacc 40

<210> SEQ ID NO 551  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 551

gpgcatgtc eggettacc ctgcccagaa tcacagctc 40

<210> SEQ ID NO 552  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

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&lt;400&gt; SEQUENCE: 552

tgagattcca gggctgggtc cacaacggcc ggcacggcc 40

&lt;210&gt; SEQ ID NO 553

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 553

ctgagtcact aacaaagctc aggcctgacc acaggacatt 40

&lt;210&gt; SEQ ID NO 554

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 554

ggctggccta cctgccacgg ggccagggtt gggcgctttc 40

&lt;210&gt; SEQ ID NO 555

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 555

gggctctgga cgctggaggc ctgaggctgc accccaggtt 40

&lt;210&gt; SEQ ID NO 556

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 556

acagtggcca ctcacccact gggcccacat cccacaggc 40

&lt;210&gt; SEQ ID NO 557

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 557

actctgccag cctttgatgc ctcgctgaga cagagggtct 40

&lt;210&gt; SEQ ID NO 558

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 558

agccggggct ctggcccat ccaggggctc cccagcagc 40

<210> SEQ ID NO 559

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 559

ccttggagt cagtcagcag gtcaggacac agttcagccc 40

<210> SEQ ID NO 560

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 560

ttacatgcag ttggtcttct cctgtgaatg gggaaactga 40

<210> SEQ ID NO 561

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 561

ctgcatcaca gaacagctgc atttctaattg tcaggcttct 40

<210> SEQ ID NO 562

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 562

cagcctggga ggcttgtaa cctccttga caagcagcc 40

<210> SEQ ID NO 563

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 563

agaaactggg gctccagggc atggaggctg cctgtggcca 40

<210> SEQ ID NO 564

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 564

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tccccgacctg gaggaagtct tattagcctc atttcatgga 40

<210> SEQ ID NO 565  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 565

tcctgccagc cccctcacgc tcacgaattc agtcccaggg 40

<210> SEQ ID NO 566  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 566

aattctaaag gtgaagggac gtctacacc ccaacaaaac 40

<210> SEQ ID NO 567  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 567

ggaaatatta gtcccctctg cctgggacaa gaccaccgaa 40

<210> SEQ ID NO 568  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 568

aaacacacct ctgaatggaa agctgagaaa cagtgatctc 40

<210> SEQ ID NO 569  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 569

actgcacccc ctcccttccc gtgccggcaa ttaaccggg 40

<210> SEQ ID NO 570  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 570

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 tgccttcta ccttgaccag tcggtccttg cgggggtccc 40

<210> SEQ ID NO 571  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

&lt;400&gt; SEQUENCE: 571

atttcttca tcttgcctt ctgacctgga gactcttcgg 40

<210> SEQ ID NO 572  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

&lt;400&gt; SEQUENCE: 572

aatgcccga aattccagca gcagcccaag atggtggcca 40

<210> SEQ ID NO 573  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

&lt;400&gt; SEQUENCE: 573

cgttgcaaat gcccaaggg gtaaccctaa aagttaaagg 40

<210> SEQ ID NO 574  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

&lt;400&gt; SEQUENCE: 574

acacaacccc tgtgcaagtt tcattccggc gcacaggggc 40

<210> SEQ ID NO 575  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

&lt;400&gt; SEQUENCE: 575

tgcaagaact aatttagcat gcaaggacgg ggaggaccgg 40

<210> SEQ ID NO 576  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

&lt;400&gt; SEQUENCE: 576

gccacgaggg cacccacgg cggacagacg gccaaagaat 40

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<210> SEQ ID NO 577  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 577  
  
accccatatc caagccggca gaatggggcg atttccaaga 40

<210> SEQ ID NO 578  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 578  
  
gcctggggag accacgagaa ggggtgactg gggcgcgggc 40

<210> SEQ ID NO 579  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 579  
  
ctgcagtagg ggacaactag gaaggccggc aggccacacg 40

<210> SEQ ID NO 580  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 580  
  
gagtgggtcc cccgggattt agggggtgag gtggaggtgg 40

<210> SEQ ID NO 581  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 581  
  
tccccgccag ggaagagggg tgcagggggc cccgtccgcc 40

<210> SEQ ID NO 582  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 582  
  
tgaggcgccg cgctgcct gcgggggagt tgccctgta 40

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<210> SEQ ID NO 583  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 583

aaacgccggg agcagcgagg ggcagagccc aaaagccatc 40

<210> SEQ ID NO 584  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 584

ttgttaagca aagatcaaag cccggcagag aatgggagcg 40

<210> SEQ ID NO 585  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 585

caacttcaac aaaactcccc tgtagtccgt gtgacgttac 40

<210> SEQ ID NO 586  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 586

ctgctactgc gccgacagcc ctctggaggc tccaggactt 40

<210> SEQ ID NO 587  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 587

gctcttctgc ccctcgccgg agcgtgcgga ctctgctgct 40

<210> SEQ ID NO 588  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 588

tccgcgctcg gctctcgctt ctgctgcccc gcgctccctc 40

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<210> SEQ ID NO 589  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 589  
  
 tttccacttc gcagcacagg agctgggtgtt ccatggctgg 40

<210> SEQ ID NO 590  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 590  
  
 ggtcggtgag gaggttgga tcgggttacg cgcggcggat 40

<210> SEQ ID NO 591  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 591  
  
 tgtcctactt caaatgtgtg cagaaggagg tctgcccgc 40

<210> SEQ ID NO 592  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 592  
  
 tcgggcccgt ctcttaagac ttccctgcaa cttgttcccc 40

<210> SEQ ID NO 593  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 593  
  
 acccacgttt cttgtact cccccctc cttctctcc 40

<210> SEQ ID NO 594  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 594  
  
 ctagaacttt gaagtttgc gtggtgttc taggatccg 40

<210> SEQ ID NO 595

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<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 595

agaagggggt cggggagggg tgccttcggg agaagccagt 40

<210> SEQ ID NO 596  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 596

caggggcacc ccaatggggc cgaggggtgcg ggctggcagg 40

<210> SEQ ID NO 597  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 597

gggtgcgctt tgtgtccccc gctgcgccc cagcccgct 40

<210> SEQ ID NO 598  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 598

gcctcagcgg cgggagccg ccaactccgg ggggaggggg 40

<210> SEQ ID NO 599  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 599

aaagtgcagt aatacccttg atcagagttg atgacttgaa 40

<210> SEQ ID NO 600  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 600

gagagaaata aagtagttgc tctatttgta aattgaaaag 40

<210> SEQ ID NO 601  
<211> LENGTH: 40

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<212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 601  
  
 ggtagcagtg attgctgtat atttgtgaaa aggaggcaag 40  
  
  
 <210> SEQ ID NO 602  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 602  
  
 tgctgataat ggaagtgcag tgggtagct ttgtttccat 40  
  
  
 <210> SEQ ID NO 603  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 603  
  
 ccggttctacc gtgactagta tgaattgtg ggaaccagaa 40  
  
  
 <210> SEQ ID NO 604  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 604  
  
 ttaacatcag tgtcaactgc agtggtggtt ctgagtaata 40  
  
  
 <210> SEQ ID NO 605  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 605  
  
 cataactcca tgctctcaaa ccaatcactc cttcattcat 40  
  
  
 <210> SEQ ID NO 606  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 606  
  
 ttctcctatg ctgcaccaga aagggttttg tgggttatca 40  
  
  
 <210> SEQ ID NO 607  
 <211> LENGTH: 40  
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 607  
  
 atcgttcagc atctttagga aatatccaga gactgcattg 40

<210> SEQ ID NO 608  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 608  
  
 tttattaaga gcaaaaaaag cctgtttcgt tagccagtca 40

<210> SEQ ID NO 609  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 609  
  
 ttgttcatat gcctaactta ataaattctt catacagaaa 40

<210> SEQ ID NO 610  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 610  
  
 ataactttta aacccaaaca cctagagatt tcattatgta 40

<210> SEQ ID NO 611  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 611  
  
 ttcttaccat taagtcttcc aaatgataat ttattataaa 40

<210> SEQ ID NO 612  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 612  
  
 tatgtaagga caacttcatt atatgcttga agaaattggt 40

<210> SEQ ID NO 613  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 613

aatcttaaaa gtgacactag tcacattcca cacggttaaa 40

<210> SEQ ID NO 614  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 614

atthtgaaaa ctatttccttt atctggaatg aatgtaaacc 40

<210> SEQ ID NO 615  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 615

ttgcattaag ggcaccagaa acttatagaa aaccaaaaag 40

<210> SEQ ID NO 616  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 616

taaaagacag tgaactgaac agtaattaac attacatcca 40

<210> SEQ ID NO 617  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 617

caaaaaactg tgthttatcat ataccaaca ttttcaagtt 40

<210> SEQ ID NO 618  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 618

tctcaggata ttttgttctc tgacacaaat acaccagtca 40

<210> SEQ ID NO 619  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 619

tagctttaca tctcagaatg aatcaatgtg ggggcagaaa 40

<210> SEQ ID NO 620  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 620

agacctatat acctatagtg cctaataagac aataagccac 40

<210> SEQ ID NO 621  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 621

tctctcccct gcctagaacta aggtaagtgg gtcttacett 40

<210> SEQ ID NO 622  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 622

catcctgctt ttaaaaccct tagtgctcag eggcttgctc 40

<210> SEQ ID NO 623  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 623

agcctataaa cttcagagta atgtagcaca aatgtctgtc 40

<210> SEQ ID NO 624  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 624

aacttgaaat aaaactttaa acgttgattg attccttccc 40

<210> SEQ ID NO 625  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 625

gacaggctta gagtccataa caaacaatct tagctggaaa 40

<210> SEQ ID NO 626  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 626

tgctcaacaa cacttggtga agagcagggc aagctatttc 40

<210> SEQ ID NO 627  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 627

ttacaacatc actgtagaca ttacttttac ccacagtgcc 40

<210> SEQ ID NO 628  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 628

atcctagtgg tatatacttc ttggataaag tatcttggta 40

<210> SEQ ID NO 629  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 629

atthttgggg agtgccattc ctgcaggtct tgaagacagg 40

<210> SEQ ID NO 630  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 630

cacacagcca atgaaactga cagagccaat gcaacaaaaa 40

<210> SEQ ID NO 631  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

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&lt;400&gt; SEQUENCE: 631

acgacttcaa tcaagagaaa caggcaggtc agagtgtgaa 40

&lt;210&gt; SEQ ID NO 632

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 632

ctggttatca gggttcatag cacatagggt tgacaaccac 40

&lt;210&gt; SEQ ID NO 633

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 633

tttattattc agctgggtaa gccaaagtgc agtcttcccc 40

&lt;210&gt; SEQ ID NO 634

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 634

gttttattct agaatcaac tgctttctaa aatgtctaa 40

&lt;210&gt; SEQ ID NO 635

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 635

tttactgatg gtacttattc cccaattat tgattattga 40

&lt;210&gt; SEQ ID NO 636

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 636

gcatttagga atattcaata ttgatactaa ggtcatcttt 40

&lt;210&gt; SEQ ID NO 637

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 637

tactctgtaa tgtagtaatc tttatgaaga aataaatttg 40

<210> SEQ ID NO 638

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 638

atdddgaaaa aatgdtttcac tgcattttac tatacaagct 40

<210> SEQ ID NO 639

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 639

accacacatt catcaaaaaa tacctcaaag aaaattctgc 40

<210> SEQ ID NO 640

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 640

gttgtcacaa taaactcagt actgagtaaa atatcacaaa 40

<210> SEQ ID NO 641

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 641

gagtatatat tgtattactt acctgatgag caaagaccca 40

<210> SEQ ID NO 642

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 642

aaaatgacag caacataggt gccacctgag gtccacatct 40

<210> SEQ ID NO 643

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 643

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tggagagagt ggggtaac tggtactaca ctttgctact 40

<210> SEQ ID NO 644  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 644

atttccatca tttgtcttt cagtaagcat gtacgaagta 40

<210> SEQ ID NO 645  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 645

gagatgaaga tggatcatca gtagggagcc cctctactgg 40

<210> SEQ ID NO 646  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 646

tctaattcat caaagtattc tgggttgatt ccaggtactg 40

<210> SEQ ID NO 647  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 647

acaaactcgt tttgtacaga gaggaaaata ttaaacacc 40

<210> SEQ ID NO 648  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 648

atgtaatta taaactcgt tataagtttt acaaatgtaa 40

<210> SEQ ID NO 649  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 649

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tccactggca gagagaatat atgtttccat tacgggccca 40

<210> SEQ ID NO 650  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 650

tcaaaggttt tctatcacgt tttctattat ttactcacat 40

<210> SEQ ID NO 651  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 651

aaaaacaaga gtcacacaac ctatgctcca caatatctgc 40

<210> SEQ ID NO 652  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 652

ataggttatt ctacaatcga caccaactat cagcggcttt 40

<210> SEQ ID NO 653  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 653

attgaattaa atgatggctt gattatccag gaatcagcca 40

<210> SEQ ID NO 654  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 654

cttaccataa cagagtaatc tctagcttat tccaaggata 40

<210> SEQ ID NO 655  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 655

acctaaaatt taactagaat cacttttcaa tgaagctgct 40

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<210> SEQ ID NO 656  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 656  
  
taaactaaga gcctttgatc ttgccttatt ctgataaaat 40

<210> SEQ ID NO 657  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 657  
  
aaataataat tcacaaggaa atccttattg tttatttaa 40

<210> SEQ ID NO 658  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 658  
  
gtaatatgta ggtaaacag aatgttgg tgaatcatgt 40

<210> SEQ ID NO 659  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 659  
  
tgcagacact aatcaaacca aacagggcca attaaaattg 40

<210> SEQ ID NO 660  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 660  
  
taaagtgcaa tgggacagag caacttcatt ttcacaaaca 40

<210> SEQ ID NO 661  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 661  
  
taatctaatt gccagaaatg cttgccatt gcaatgggag 40

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<210> SEQ ID NO 662  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 662  
agttgacaat gactgcttag tttagggttt tgaagtaaac 40

<210> SEQ ID NO 663  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 663  
cagatggcag gtattctgtg aattaacact gatgcttctg 40

<210> SEQ ID NO 664  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 664  
agtcaagttc agaaatgatc tgttatgacc ccatgaaacg 40

<210> SEQ ID NO 665  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 665  
gggatgctct gatacatcat tcagtaaaat gatagaaaa 40

<210> SEQ ID NO 666  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 666  
tagctgtatt gcttgatagc ttcatagctt gataaccatt 40

<210> SEQ ID NO 667  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 667  
ttttagcagg gaattaacac aggtatataa atgaagaaaa 40

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<210> SEQ ID NO 668  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 668

ttgattgttt atgaagctga gattgtttac tggtttcgag 40

<210> SEQ ID NO 669  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 669

tctgtgtttt tatgtttggg aacatgaggg aatcagttct 40

<210> SEQ ID NO 670  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 670

ttcttaagct ttcatttttc cagtggtgaa tgtagagaga 40

<210> SEQ ID NO 671  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 671

acggtaactg aataaactta agaactgagg taaagttttc 40

<210> SEQ ID NO 672  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 672

tcaatatgta aaattgatca attcagacac ctttatatgg 40

<210> SEQ ID NO 673  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 673

tgctcttttc atgctgtaaa tagagcattg catgaaagat 40

<210> SEQ ID NO 674

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<211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 674  
  
 ttcatagcac agtttataaa cctaagaaag caaagatgaa 40

<210> SEQ ID NO 675  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 675  
  
 aaccaagcag gattctatga ctaaaaaagt gtatttgat 40

<210> SEQ ID NO 676  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 676  
  
 agatagagaa tttcaaagaa accatcttta tcagctgcac 40

<210> SEQ ID NO 677  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 677  
  
 ccaagaatga aaagatgcac taattcgact gaaagccaag 40

<210> SEQ ID NO 678  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 678  
  
 tcatagttga gacatataac aaccataaag gtccgcatat 40

<210> SEQ ID NO 679  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 679  
  
 aggaaagggt ggaaaggcaa gcagcgggga gtggtggctg 40

<210> SEQ ID NO 680  
 <211> LENGTH: 40

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<212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 680  
  
 ctataaattg acctatcctg taaaaaagga tgtcacagca 40  
  
 <210> SEQ ID NO 681  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 681  
  
 acaattgacc taagactgta aattgtaaat tgactataaa 40  
  
 <210> SEQ ID NO 682  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 682  
  
 gcaagactgg gtatactatt aataggaaaa aatgaacttc 40  
  
 <210> SEQ ID NO 683  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 683  
  
 attgctttga tattgattga atcacagaga aaatcctaag 40  
  
 <210> SEQ ID NO 684  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 684  
  
 tagattatgc tggcaaatct cagtgatcag agaattatat 40  
  
 <210> SEQ ID NO 685  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 685  
  
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 <210> SEQ ID NO 686  
 <211> LENGTH: 40  
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 686  
  
 gtttgaatta ttattcaaac agtgtatggt tgtttgtact 40  
  
 <210> SEQ ID NO 687  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 687  
  
 aatgcaacag agacaggat ttatagcatc tgttttccat 40  
  
 <210> SEQ ID NO 688  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 688  
  
 tttaatatcc aaatagtgtat ggacacatac aattgtacat 40  
  
 <210> SEQ ID NO 689  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 689  
  
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 <210> SEQ ID NO 690  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 690  
  
 ggagcgcctcc tgcgcgcctt gttcgttagg atttatTTTT 40  
  
 <210> SEQ ID NO 691  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
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 ggtggctccc taatgcctgc tegtttcagg tctcagctct 40  
  
 <210> SEQ ID NO 692  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 692

ccttagtggtg ttgaggacgc tgcagaaggt acagaggaga 40

<210> SEQ ID NO 693  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 693

gaccagatgg taggacagtc attctcctct cgcgtctccgc 40

<210> SEQ ID NO 694  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 694

cgtgaggcat ggagtttttg tcttgcccct gcctgggtag 40

<210> SEQ ID NO 695  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 695

tttaagtctc tggcaccgtg catagcagaa ttggttgga 40

<210> SEQ ID NO 696  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 696

tctttctcca agtgctctta tgtggcaca tctctgaaat 40

<210> SEQ ID NO 697  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 697

tgcgtcccg ccaggaagc agcttccctc tcagctgcct 40

<210> SEQ ID NO 698  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 698

gggtgtatgt agctggcaga agtgggactt ggtcgcaacc 40

<210> SEQ ID NO 699  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 699

cgtggcgagt gggcggtagc tgctcgtaga gcgtgtgaaa 40

<210> SEQ ID NO 700  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 700

gttggcccta aaagtatca ttcatgctag ttgaccaat 40

<210> SEQ ID NO 701  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 701

aagtgggagg agctgggcaa gaaagtccac ccccttttct 40

<210> SEQ ID NO 702  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 702

gccgagccga agtcatctgc caatcaaac agccacaggg 40

<210> SEQ ID NO 703  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 703

cgcgtaacct atgggagaca gacaggtgcc tttaaagcgg 40

<210> SEQ ID NO 704  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 704

tggggaaagc ggaggaaggc atggagtgtg ggcgttaggg 40

<210> SEQ ID NO 705  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 705

gcattattctg ccttgaagtc attggttggt cctggaagtg 40

<210> SEQ ID NO 706  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 706

aattggtctg ggggaggagc tacgacagtc caggggcggg 40

<210> SEQ ID NO 707  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 707

gtgtcgtgct gattggatgt atccgcccc ctctcttaaa 40

<210> SEQ ID NO 708  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 708

caacacgcca gcgcgaggac ccgaacgtca atcaagagac 40

<210> SEQ ID NO 709  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 709

gcgttcgatt ggctcccgcc gcaggetgct aggattggct 40

<210> SEQ ID NO 710  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

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&lt;400&gt; SEQUENCE: 710

ccctgcccc tttcgcggat tgggtgatcg ctccaaggcg 40

&lt;210&gt; SEQ ID NO 711

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 711

ctgacccttg gaggtttct attggttct ggcagggatg 40

&lt;210&gt; SEQ ID NO 712

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 712

tcccgaatat aggccagtca ttgctctgc tgaacgtgc 40

&lt;210&gt; SEQ ID NO 713

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 713

cccctcctct cttctcgtct ctggcgccga cccgcccccg 40

&lt;210&gt; SEQ ID NO 714

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 714

gctcaaggga ggcccgggcg tctgccgatg gctccggga 40

&lt;210&gt; SEQ ID NO 715

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 715

tgggggagtg ggccccgggt tgttctgacg acgggggtcg 40

&lt;210&gt; SEQ ID NO 716

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 716

cccgggcgct atcgcgatag cggcgcgaag cggaagtggg 40

<210> SEQ ID NO 717

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 717

cgggggaggc gagcgcccgc cgcctttttc tcgcgcccgc 40

<210> SEQ ID NO 718

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 718

cacaggagct ggcgcccgcg ctgaggagcg tategcgaca 40

<210> SEQ ID NO 719

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 719

gttgccgact cgcgctctcg gcttctgctc eggggcttct 40

<210> SEQ ID NO 720

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 720

actcggagct cggatcccag tgtggacctg gactcgaatc 40

<210> SEQ ID NO 721

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 721

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<210> SEQ ID NO 722

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 722

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ctttccggag cccgtctgtt ccccttcggg tccaaagctt 40

<210> SEQ ID NO 723  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 723

gaccccgct cattcctcac ggcgagctcc agaccccgcc 40

<210> SEQ ID NO 724  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 724

agaactcaag ctcccgattg tgcccgaagg aacccgaagg 40

<210> SEQ ID NO 725  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 725

actattgccc aagtgcgccc aagtttgctg ccccgttccc 40

<210> SEQ ID NO 726  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 726

acatgtggct cgcgccacac tggcctcagc tctccgttct 40

<210> SEQ ID NO 727  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 727

acagtgaccc taaggactcg actacctccg aagaaagccc 40

<210> SEQ ID NO 728  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 728

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 cttgtacca actatctacg aagtaaaccg aagcttgtgg 40

<210> SEQ ID NO 729  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 729

tatctggcga acctgttgac tccgcctatc atcctagcgt 40

<210> SEQ ID NO 730  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 730

ggcaagtcgc ttctgccccg cccccttgta aatactcatg 40

<210> SEQ ID NO 731  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 731

ctctctact tgggaacttg aggatcgca cctggccccg 40

<210> SEQ ID NO 732  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 732

ttggtccgc cccactgagc gcacctccct ctgccgttc 40

<210> SEQ ID NO 733  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 733

tccttgetcc accccctcat gccgacacc tcgtcaactt 40

<210> SEQ ID NO 734  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 734

tccaccgata gaaccagcga gtcacctcat aaacagtaat 40

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<210> SEQ ID NO 735  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 735  
  
cgctcagtcc gcctccttgc ctcccctcag aatgtcccac 40

<210> SEQ ID NO 736  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 736  
  
gccgtccact ctccgctcgg gcgggctcac cccaattggg 40

<210> SEQ ID NO 737  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 737  
  
cgaccgaacc ccacagccga aagccccgcc ccttggacac 40

<210> SEQ ID NO 738  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 738  
  
ctccgagcgc cagcgcaccc cagtgggga gttcccggcc 40

<210> SEQ ID NO 739  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 739  
  
agccccgcct cctcccggac gcaataggtt cggcgttcgg 40

<210> SEQ ID NO 740  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 740  
  
agcaatttga cgttcgggtg ttctcggctc ggccgaatcc 40

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<210> SEQ ID NO 741  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 741

tgccccctcc cgagcacagg aagttcggcg ttcgggcgtc 40

<210> SEQ ID NO 742  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 742

tttcggacct cctcgctctc agactccac agtacaaaac 40

<210> SEQ ID NO 743  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 743

cgagccttgc ctctctctct ttccgaacga ctgtgattcg 40

<210> SEQ ID NO 744  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 744

gaggctaagg caccgccgag gccacaccct cttccggacg 40

<210> SEQ ID NO 745  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 745

gcgtccccct tcgggtgttc ccgtcagcgg tcagaagctc 40

<210> SEQ ID NO 746  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 746

ccttacaag gtccattttg gcaccaccct cttgcaaagt 40

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<210> SEQ ID NO 747  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 747  
  
ggagcgtgaa aaacaaacct ccgcaagcgc ggcgacacgc 40

<210> SEQ ID NO 748  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 748  
  
acccgctctg tgcccgcact gccgtacctt ccattgcgcc 40

<210> SEQ ID NO 749  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 749  
  
ggctctcagc atctgcatat gtagccctc ccgctggatc 40

<210> SEQ ID NO 750  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 750  
  
cccaaccctt accccaatc catcttagag ctgattctct 40

<210> SEQ ID NO 751  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 751  
  
actccagtga ttcttcctta tgctaggac tcgaggaccc 40

<210> SEQ ID NO 752  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 752  
  
gagaattgag aagtcagtgt gggaggggat gtcccagtac 40

<210> SEQ ID NO 753

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<211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 753  
  
 tttctggttc gcgttggtg cattgtggag ctgagggatg 40

<210> SEQ ID NO 754  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 754  
  
 tagcttctta atctccttct ttaggtcagc ctcatacttt 40

<210> SEQ ID NO 755  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 755  
  
 ttctccctgg gaccagcag tccactctcc cagttccctc 40

<210> SEQ ID NO 756  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 756  
  
 aaagtcagac ctcaggaccc aggaactggg gccacagct 40

<210> SEQ ID NO 757  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 757  
  
 tcttgatttg gtcctcagc cgtgcagat gggaaaagca 40

<210> SEQ ID NO 758  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 758  
  
 taagtgctt cttgtccttg atctcgttgg acgctacca 40

<210> SEQ ID NO 759  
 <211> LENGTH: 40

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<212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 759  
  
 ggctctgggc tcctaccgct tcaatgagct tgcggttgct 40  
  
  
 <210> SEQ ID NO 760  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 760  
  
 tgaggacctc tggggtctgg ccgctctgcc tccgccctt 40  
  
  
 <210> SEQ ID NO 761  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 761  
  
 ctgcctcttc acttccctta ggtgcagaaa ccttacttct 40  
  
  
 <210> SEQ ID NO 762  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 762  
  
 cgacctgagc ctctgaccc tactttctga gctctgagtc 40  
  
  
 <210> SEQ ID NO 763  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 763  
  
 tcaaaggtgg gaaaggagct gactaagggc cagcagacac 40  
  
  
 <210> SEQ ID NO 764  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 764  
  
 ccgttcatt tgctgtagag agtgcagttg gcaggggggc 40  
  
  
 <210> SEQ ID NO 765  
 <211> LENGTH: 40  
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 765  
  
 gctgtaagct ttggttttgg tctctcggtc cacaactttg 40  
  
 <210> SEQ ID NO 766  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 766  
  
 ccaactcacc gtgagccact ggccaacctc ttccttctcc 40  
  
 <210> SEQ ID NO 767  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 767  
  
 ccagggtca ggttcctcag agttcacctc ctcttctcta 40  
  
 <210> SEQ ID NO 768  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 768  
  
 gtccacctgc atgttgagcg tgtcgatggt attctagggg 40  
  
 <210> SEQ ID NO 769  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 769  
  
 gcgtgtctgc actgacagtg actccacttc actctcaaac 40  
  
 <210> SEQ ID NO 770  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 770  
  
 tgtegggtct ccctcaactca catccttctgc gcccttcttc 40  
  
 <210> SEQ ID NO 771  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 771

ctgctggcca gcccattoce atgcccattcc ccatcccaaa 40

<210> SEQ ID NO 772  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 772

gaatccaggc cccaactccc aggagcataa atgactggcc 40

<210> SEQ ID NO 773  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 773

tctcaaatcc ctaatcccgg ctgttggccc tgtccgcctg 40

<210> SEQ ID NO 774  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 774

cctgccccac gcgtgcagct gctaagccct cccaatcctg 40

<210> SEQ ID NO 775  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 775

cccagacacc caggggaccc tgagattctg tctgacctcc 40

<210> SEQ ID NO 776  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 776

cttcccccaa gtcgctctc ttcacaaagg ccccacggtc 40

<210> SEQ ID NO 777  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 777

cctctgggtg ccaggaggcc tcttgccatg ggtgtccttc 40

<210> SEQ ID NO 778

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 778

ctgccttgtc tctaccact gtgctctccc taggaccagg 40

<210> SEQ ID NO 779

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 779

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<210> SEQ ID NO 780

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 780

tgcgctcgat ctcaccttc agttcgtagc ccacctgggg 40

<210> SEQ ID NO 781

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 781

tcacctgctt cacaggcggc ggctcctgcc acttgctgaa 40

<210> SEQ ID NO 782

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 782

ctcgcttett ccgctgtcca tccaggggcg caggcagcgg 40

<210> SEQ ID NO 783

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 783

cccatgccta cggaccgcc agggcccctc acctgcggcc 40

<210> SEQ ID NO 784  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 784

agtcggctgg gaggaggacg ccggcttctc cctccatga 40

<210> SEQ ID NO 785  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 785

atcttgcggt acctggggac gggtggtgg gcggcgccag 40

<210> SEQ ID NO 786  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 786

ttggcctgct tccggatctc cgtcagcccc agccgctcct 40

<210> SEQ ID NO 787  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 787

ggagggcgct ctgggagtct gacctctccg aagctcatac 40

<210> SEQ ID NO 788  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 788

aggaggcaga gggcggtggc ggtggctgg ctgtggggtt 40

<210> SEQ ID NO 789  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

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&lt;400&gt; SEQUENCE: 789

agacatgagc cagggccaca ggacgagagg aggggcggtg 40

&lt;210&gt; SEQ ID NO 790

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 790

ccaagggcgc cgagggctgc tttggggctg aatggatgga 40

&lt;210&gt; SEQ ID NO 791

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 791

gatgggaagc cgcgggggct ctaagcagcg gagacacagg 40

&lt;210&gt; SEQ ID NO 792

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 792

ggagcctctg ggcagggagg aaccggccaa ggagcccggg 40

&lt;210&gt; SEQ ID NO 793

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 793

ggcggggccc agggacgggg cggccgtgca gcagggcact 40

&lt;210&gt; SEQ ID NO 794

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 794

ctgcaggacc aaggggatga cgctgggata acagaggaga 40

&lt;210&gt; SEQ ID NO 795

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 795

cagaacaggt ttaataggat gaggtggcct ctgagttcgg 40

<210> SEQ ID NO 796

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 796

ccattccttc cttactcgtg tgggtcgggg gatgtcagga 40

<210> SEQ ID NO 797

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 797

ggcccgggtcc cagcaactgct ctgtgagctc agagttggga 40

<210> SEQ ID NO 798

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 798

tggggggccca cacacgcggg ggatgccggg gagcctgaga 40

<210> SEQ ID NO 799

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 799

cacgggcacc tgetccggta cccactcggc cgggctgagg 40

<210> SEQ ID NO 800

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 800

ctccaccagc cggaagccca gcggtcacca gccggccggt 40

<210> SEQ ID NO 801

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 801

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aggcgctctc ctcgatctag ggggaagagg aggcgccctg 40

<210> SEQ ID NO 802  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 802

acttgcccag gtggcccagg ctgaatccca ggtcctcctg 40

<210> SEQ ID NO 803  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 803

tggcctcggt tacctgtgtc tgccgcacac gcccaactgcc 40

<210> SEQ ID NO 804  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 804

gtctggccca tacctgcagc gtcttggaga tcttggcctt 40

<210> SEQ ID NO 805  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 805

gtcccccca ccttgtgtcc ctcggtcccc agccccacct 40

<210> SEQ ID NO 806  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 806

tgcagggtcc gctgtgggga ggacaggag gctgcgatct 40

<210> SEQ ID NO 807  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 807

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tcgcggatgg tggacttccc gccatatacg acgctctgct 40

<210> SEQ ID NO 808  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 808

agtgggggtga aggccacgct ggaggccgtg cccgaggagc 40

<210> SEQ ID NO 809  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 809

eggctgctga gcctaaccac ctectgggct tctttccagc 40

<210> SEQ ID NO 810  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 810

gctcatggta tccctaccgc aggcaatctg tggacagcac 40

<210> SEQ ID NO 811  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 811

ctgaatgtca cctgaagggt cacagaagct actcacaggg 40

<210> SEQ ID NO 812  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 812

ttaagtgttc tcaatatgag attagctgga gccgcctaat 40

<210> SEQ ID NO 813  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe

<400> SEQUENCE: 813

gaagatccat ctgttgaag ccagaggact agtgggaaac 40

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<210> SEQ ID NO 814  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 814  
  
ccccacagg gatctgacac acaacttagg ttgtcagcca 40

<210> SEQ ID NO 815  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 815  
  
gccagcttc ccaagtctg cctggacacc gccccatgga 40

<210> SEQ ID NO 816  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 816  
  
aatcaccttc atgcttaaaa cactcacact gattccagc 40

<210> SEQ ID NO 817  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 817  
  
cctcttgggg acctgggtga ccttactcac cctcatggct 40

<210> SEQ ID NO 818  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 818  
  
gttgctgtgg acaggcttgg agccgttttt ggctggagac 40

<210> SEQ ID NO 819  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 819  
  
ggagggtag gtggcgcca cagctgggga ctgaggggtgc 40

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<210> SEQ ID NO 820  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 820

gccaggagtg gtgctcaagg cagaggcagc aggcgggggg 40

<210> SEQ ID NO 821  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 821

cagggcactt gggggtgctg cgggggctgg gaccccattg 40

<210> SEQ ID NO 822  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 822

ggtgcccag ttgtggctgg gagctggact ggccttgggg 40

<210> SEQ ID NO 823  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 823

ctgcttgcca gccctccac cggcactgct gttactactg 40

<210> SEQ ID NO 824  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 824

gcccccaacc ccgctgcctc ctactcaact ggtggcgcca 40

<210> SEQ ID NO 825  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 825

gggctgtct gccacaactg agctgtaacc tggaacaaa 40

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<210> SEQ ID NO 826  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 826

gctggcattg ttgccccac tgetgetcaa agccacctct 40

<210> SEQ ID NO 827  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 827

aggtgggttg tgggggcccg aagggggcc caaggcctgg 40

<210> SEQ ID NO 828  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 828

tccaaccct gccgatggcc gagacactca cgaggtgctg 40

<210> SEQ ID NO 829  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 829

gggggtgagg cgctgcgcc tctctgttc aaaaggctgc 40

<210> SEQ ID NO 830  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 830

attcccagca gcaagggcgg ggggttcaga acccaccgat 40

<210> SEQ ID NO 831  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 831

gggggtgtaa caccggagg agatggagga tagcgcttgg 40

<210> SEQ ID NO 832

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<211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 832  
  
 caaagcaggg aggctgatgt agtttccttg ctggaagaa 40

<210> SEQ ID NO 833  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 833  
  
 cttccactta gatgagaacg tatttttagaa tgttctgaag 40

<210> SEQ ID NO 834  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 834  
  
 taacagaaat ggggaggaaa gggatatggg ctcttgagaa 40

<210> SEQ ID NO 835  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 835  
  
 aaacagtgac cctccggtgg cagtcaattg gcctcaggca 40

<210> SEQ ID NO 836  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 836  
  
 gcagaggaat aaggacttcg ggacaattca ctttgaaaag 40

<210> SEQ ID NO 837  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 837  
  
 gaccagtgga aatggtctga gctaagattt gaaggagtgg 40

<210> SEQ ID NO 838  
 <211> LENGTH: 40

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 838

tgcacactga tctttcttag ggcattcttc gggaaacagg 40

<210> SEQ ID NO 839  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 839

ggctcaggat gaacagcaac aggggttggg atgatcactg 40

<210> SEQ ID NO 840  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 840

gatcatggag atgtgatcta ggaacaaaag ccagagaagg 40

<210> SEQ ID NO 841  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 841

aggcattccc acggtgtgag gtcagattgg gcagggccta 40

<210> SEQ ID NO 842  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 842

agagccagca cttgctgttc cacacatact agatcagtct 40

<210> SEQ ID NO 843  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 843

tggacaaccc cctccacac ccagagctgt ggaaggggag 40

<210> SEQ ID NO 844  
<211> LENGTH: 40  
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 844  
  
cacctagatg ctgaccaagg cctccccat gctgctggag 40  
  
<210> SEQ ID NO 845  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 845  
  
ataaagcctt cattctccag gacccccgcc ttgcctgtt 40  
  
<210> SEQ ID NO 846  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 846  
  
aggtggtgag tttggggctg gggggcctcc ctgaggagcc 40  
  
<210> SEQ ID NO 847  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 847  
  
gagagaacca ggtccacat gctgacacag gtgtccacgg 40  
  
<210> SEQ ID NO 848  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 848  
  
atcccccaa tctcaccagt gcacccccaca gacaaggcga 40  
  
<210> SEQ ID NO 849  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 849  
  
aagggttca gcataagagt cagaaccgc ccccttct 40  
  
<210> SEQ ID NO 850  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 850

tgtgggctga agggacgagg ctggggcact ggggtgggagg 40

<210> SEQ ID NO 851  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 851

ttgcaatgtg gaagagtcag gggcacattg tctgggctga 40

<210> SEQ ID NO 852  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 852

taagtgggag ggagcgggga cctagtgtgg gcatgaggac 40

<210> SEQ ID NO 853  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 853

ggagcagggga tttggctggg caatggagag aaaggtctga 40

<210> SEQ ID NO 854  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 854

acacagagat gcccaggaac ttgctcttta gtaaagcagc 40

<210> SEQ ID NO 855  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 855

tggagagagg tccttgaaag gttttgaacc ccataaagag 40

<210> SEQ ID NO 856  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 856

tcaggaggca gccccagtgat agggccaag gaaccagtgg 40

<210> SEQ ID NO 857  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 857

acagtctact gacttttctc attcagctgt gagcattcaa 40

<210> SEQ ID NO 858  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 858

ctgtccctg gaccttgaca cctggctccc caaccctgtc 40

<210> SEQ ID NO 859  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 859

aggaaacca gattccacca gacacttctc tcttccccc 40

<210> SEQ ID NO 860  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 860

ggctatctgg cctgagacaa caaatgctgc ctcccacct 40

<210> SEQ ID NO 861  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 861

gtctggcact gggactttca gaactcctcc ttccctgact 40

<210> SEQ ID NO 862  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 862

ttgcccaga cccgtcattc aatggctagc tttttocatg 40

<210> SEQ ID NO 863  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 863

aaaaacacga gcaccccaaa ccacaacggc cagttctctg 40

<210> SEQ ID NO 864  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 864

ttaaccttgg acatggtaaa ccatccaaaa ccttcctctc 40

<210> SEQ ID NO 865  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 865

agcaactaaa cctctccact gggcacttat ccttggtttc 40

<210> SEQ ID NO 866  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 866

gaaccttcta ttctcttaga acccacagct gccaccacag 40

<210> SEQ ID NO 867  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 867

tcccttctcc cagtgaaga ccccaaatca ctccaaatga 40

<210> SEQ ID NO 868  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

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&lt;400&gt; SEQUENCE: 868

caacccccaa cccgatgcct gcttcagatg tttcccatgt 40

&lt;210&gt; SEQ ID NO 869

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 869

cataaacctg gctcctaaag gctaaatatt ttgttgagga 40

&lt;210&gt; SEQ ID NO 870

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 870

ctgctgacct gccctcccag gtcagaatca tctcatgca 40

&lt;210&gt; SEQ ID NO 871

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 871

tgttctccag acctgtgcac tctatctgtg caacagagat 40

&lt;210&gt; SEQ ID NO 872

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 872

cgtgcagcaa acaatgtgga attccaataa cccccactc 40

&lt;210&gt; SEQ ID NO 873

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

&lt;400&gt; SEQUENCE: 873

aaatatgagt ctcccaagt tccttagcat ttcaaatcc 40

&lt;210&gt; SEQ ID NO 874

&lt;211&gt; LENGTH: 40

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 874

catcataaaa agatcttgtg gtccacagat cctctagccc 40

<210> SEQ ID NO 875

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 875

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<210> SEQ ID NO 876

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 876

cactctgaga ccagaaacta gaacttttat tcctcatgct 40

<210> SEQ ID NO 877

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 877

caccagcact caggagattg tgagactccc tgatccctgc 40

<210> SEQ ID NO 878

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 878

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<210> SEQ ID NO 879

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 879

gggggtgggt acgatccccg attcttcata caaagcctca 40

<210> SEQ ID NO 880

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 880

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ggacaaaggc agaggagaca cgcccaggat gaaacagaaa 40

<210> SEQ ID NO 881  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 881

tggatgcacc aggcctgta gctcatggag acttcatcta 40

<210> SEQ ID NO 882  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 882

gggagagcta gcacttgctg ttctgcaatt actagatcac 40

<210> SEQ ID NO 883  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 883

ggctggacaa cccctccca caccagagc tgtggaaggg 40

<210> SEQ ID NO 884  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 884

tggcaccagc aggctgacca aggcctccc catgctgctg 40

<210> SEQ ID NO 885  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 885

cctataaac cttcattccc caggactccg cccctgcct 40

<210> SEQ ID NO 886  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 886

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tgcaggtggt aagcttgggg ctggggagcc tccccagga 40

<210> SEQ ID NO 887  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 887

aggaagacaa cggggaccca catggtgaca cagctctccg 40

<210> SEQ ID NO 888  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 888

caacatggc ccctctcacc aatccacgtc acggacaggg 40

<210> SEQ ID NO 889  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 889

tcagcttgac agtcagggtt ggctccctct cctgcatccc 40

<210> SEQ ID NO 890  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 890

tcctgtctg ggctgggggt ctgggttggg ggggaagag 40

<210> SEQ ID NO 891  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 891

tgtgggagtg aggactgttg caatatggag gggctggggg 40

<210> SEQ ID NO 892  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 892

gggagaaagt tctggggtaa gtgggagga gcggggacct 40

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<210> SEQ ID NO 893  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 893  
  
ttgtggggct caaacctcc aaggacctct ctcaatgccca 40

<210> SEQ ID NO 894  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 894  
  
tgcccaaccc tateccagag accttgatgc ttggcctccc 40

<210> SEQ ID NO 895  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 895  
  
tcttgcccta ggataccag atgccaacca gacacctcct 40

<210> SEQ ID NO 896  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 896  
  
ttcctagcca ggctatctgg cctgagacaa caaatgggtc 40

<210> SEQ ID NO 897  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 897  
  
tcttagcccc agactcttca ttcagtggcc cacattttcc 40

<210> SEQ ID NO 898  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 898  
  
aggaaaaaca tgagcatccc cagccacaac tgccagctct 40

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<210> SEQ ID NO 899  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 899

ccccttcaga gttactgaca aacaggtggg cactgagact 40

<210> SEQ ID NO 900  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 900

tggaaagtta gcttatttgt ttgcaagtca gtaaaatgtc 40

<210> SEQ ID NO 901  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 901

gactcaggag tctcatggac tctgccagca ttcacaaaac 40

<210> SEQ ID NO 902  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 902

atgctgtctg ctaagctgtg agcagtaaaa gcctttgcct 40

<210> SEQ ID NO 903  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 903

gatttggggg gggcaaggtg tactaatgtg aacatgaacc 40

<210> SEQ ID NO 904  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 904

gtgtgcacag catccaccta gactgctctg gtcaccctac 40

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<210> SEQ ID NO 905  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 905

aggattccta atctcaggtt tctcaccagt ggcacaaaacc 40

<210> SEQ ID NO 906  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 906

caaaggctga gcaggtttgc aagttgtccc agtataagat 40

<210> SEQ ID NO 907  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 907

gtcaaggaca atcgatacaa tatgttctc cagagtaggt 40

<210> SEQ ID NO 908  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 908

gcaagatgat atctctctca gatccaggct tgcttactgt 40

<210> SEQ ID NO 909  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 909

tctgtgtgtc ttctgagcaa agacagcaac accttttttt 40

<210> SEQ ID NO 910  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 910

aacgttgaga ctgtcctgca gacaaggggtg gaaggctctg 40

<210> SEQ ID NO 911

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<211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 911  
  
 cataaataag caggatgtga cagaagaagt atttaatggt 40  
  
 <210> SEQ ID NO 912  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
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 gctgccagac acagtcgatc gggacctaga accttggtta 40  
  
 <210> SEQ ID NO 913  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 913  
  
 gggatcctga gcgctgcctt attctgggtt tggcagtgga 40  
  
 <210> SEQ ID NO 914  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 914  
  
 tcactcaaac ccagaagttc tgatccccag ccatgccctt 40  
  
 <210> SEQ ID NO 915  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 915  
  
 agcctcttcc tcctttgaaa ttcaagaggg tggaccctt 40  
  
 <210> SEQ ID NO 916  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 probe  
  
 <400> SEQUENCE: 916  
  
 ggagctggga ccttaccagt ctctccctc attgacctaa 40  
  
 <210> SEQ ID NO 917  
 <211> LENGTH: 40

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<212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 917  
 gaggatatga gattcttagg ccattccac atcagtacct 40

<210> SEQ ID NO 918  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 918  
 taccagaac tctaccctc aggattccag caccttcttc 40

<210> SEQ ID NO 919  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 919  
 gcctctgccc ttcaggggcc aaagagcctt aagccacaaa 40

<210> SEQ ID NO 920  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 920  
 atcccattac taccacca aacctggac ctaatggttc 40

<210> SEQ ID NO 921  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 921  
 aatgggcaac cctcgatcct cagactcttg aggaatcaag 40

<210> SEQ ID NO 922  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
 <400> SEQUENCE: 922  
 gataccctca agtggagtaa ggattagtg gcaagatgga 40

<210> SEQ ID NO 923  
 <211> LENGTH: 40  
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 923  
gtgcttgccc aggggcacct tcatggagct agaagggctg 40

<210> SEQ ID NO 924  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 924  
gatgacaccc aaggcctctg gggcatcttt catgctcaga 40

<210> SEQ ID NO 925  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 925  
tgctggccac accctcagag tgtggatgct ggatgatgag 40

<210> SEQ ID NO 926  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 926  
gaggcacgct gcagggatag tcacagcaac atgacgtcat 40

<210> SEQ ID NO 927  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 927  
agaggaggat gtcggcagct ctacggttgg caggtggctg 40

<210> SEQ ID NO 928  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe  
  
<400> SEQUENCE: 928  
gacactaggc ctcagcctgg caccatgcag gccactccca 40

<210> SEQ ID NO 929  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 929

acttttgagt cctggatccc tatgattcca ggctccctgt 40

<210> SEQ ID NO 930  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 930

ccttgagatt tcatggatgg tgacatatgg ccattcteta 40

<210> SEQ ID NO 931  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 931

aaaaccata agttcaggtc cctgtgccct ccaccagaa 40

<210> SEQ ID NO 932  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 932

tcgtatctgg gagactcact tgggagagca atagacttgg 40

<210> SEQ ID NO 933  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 933

tacaagatgt ggtggagata aggctgatgc tggcacagtg 40

<210> SEQ ID NO 934  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 934

gtacacacca tgggtttcat cagggccctg ggtagtcct 40

<210> SEQ ID NO 935  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 935

gctgtgacct cacaggagtc cgtgcctcca cccctactc 40

<210> SEQ ID NO 936  
 <211> LENGTH: 16  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 936

cgtcgcacca agaaat 16

<210> SEQ ID NO 937  
 <211> LENGTH: 16  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 937

tagacttgcc atacgt 16

<210> SEQ ID NO 938  
 <211> LENGTH: 16  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 938

aattcttgag accagg 16

<210> SEQ ID NO 939  
 <211> LENGTH: 16  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 939

atctgccc aa actcca 16

<210> SEQ ID NO 940  
 <211> LENGTH: 16  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 940

ttccaagcg tcattc 16

<210> SEQ ID NO 941  
 <211> LENGTH: 16  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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oligonucleotide

<400> SEQUENCE: 941

tctatcggac gctgta 16

<210> SEQ ID NO 942  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> SEQUENCE: 942

aaaaaaaaa atttcttggg gcgacg 26

<210> SEQ ID NO 943  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> SEQUENCE: 943

aaaaaaaaa acgtatggca agtcta 26

<210> SEQ ID NO 944  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> SEQUENCE: 944

aaaaaaaaa cctggtctca agaatt 26

<210> SEQ ID NO 945  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> SEQUENCE: 945

aaaaaaaaa tggagtttgg gcagat 26

<210> SEQ ID NO 946  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> SEQUENCE: 946

aaaaaaaaa agatgacgct tgggaa 26

<210> SEQ ID NO 947  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
oligonucleotide

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<400> SEQUENCE: 947

aaaaaaaaa tacagcgtcc gataga

26

<210> SEQ ID NO 948

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 948

atztatagaa accgggggcg aaaaaacgta tggcaagtct a

41

<210> SEQ ID NO 949

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 949

cgaacaggag gagcagagag aaaaaacgta tggcaagtct a

41

<210> SEQ ID NO 950

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 950

gctggcgacg caaagaaga aaaaaacgta tggcaagtct a

41

<210> SEQ ID NO 951

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 951

catggtgtct gagcgtgtg aaaaaacgta tggcaagtct a

41

<210> SEQ ID NO 952

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 952

tacgacaaa tccgttgact aaaaaacgta tggcaagtct a

41

<210> SEQ ID NO 953

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 953

caagtgtaaa agcagccctg aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 954

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 954

gggtcattga tggcaacaat aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 955

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 955

aaccatgtag ttgaggtaaa aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 956

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 956

gggtggaatc atattggaac aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 957

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 957

ttgacggtgc catggaattt aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 958

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 958

cattgatgac aagcttcccg aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 959

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 959

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tcttggaaga tggatgagg aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 960  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 960

ccacttgatt ttggaggat aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 961  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 961

ggactccaag acgtactcag aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 962  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 962

ttctccatgg tgggaagac aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 963  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 963

agagatgatg acccttttgg aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 964  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 964

gacgaacatg ggggcatcag aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 965  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 965

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catacttctc atggttcaca aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 966  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 966

attgctgatg atcttgaggc aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 967  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 967

ctaagcagtt ggtggcgag aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 968  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 968

ccacgatacc aaagttgtca aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 969  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 969

tcttctgggt ggcagtgatg aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 970  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 970

tagaggcagg gatgatgttc aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 971  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 971

tcagctcagg gatgacctg aaaaaacgta tggcaagtct a 41

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<210> SEQ ID NO 972  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 972  
  
cactgacaagc ttggcagtg aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 973  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 973  
  
caggtttttc tagacggcag aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 974  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 974  
  
caccttcttg atgtcatcat aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 975  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 975  
  
gctgttgaag tcagaggaga aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 976  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 976  
  
cgtcaaaggt ggaggagtgg aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 977  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe  
  
<400> SEQUENCE: 977  
  
agtggtcggt gagggcaatg aaaaaacgta tggcaagtct a 41

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<210> SEQ ID NO 978  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 978

tcataccagg aaatgagctt aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 979  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 979

cctgttgctg tagccaaatt aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 980  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 980

tgaggagggg agattcagtg aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 981  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 981

ctcttcaagg ggtctacatg aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 982  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 982

tacatgacaa ggtgcggtc aaaaaacgta tggcaagtct a 41

<210> SEQ ID NO 983  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 983

tgagcacagg gtactttatt aaaaaacgta tggcaagtct a 41

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<210> SEQ ID NO 984  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 984

aggagtatga ttgtcaaccc aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 985  
<211> LENGTH: 40  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 985

cctatataag gcgaagcaca aaaatggagt ttgggcagat 40

<210> SEQ ID NO 986  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 986

gagtgactcg agagagctac aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 987  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 987

atagtgagca acgtaggctt aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 988  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 988

ggacatgagt tggcaattt aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 989  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 989

gagatcaact cccgaaggaa aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 990

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<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 990

aatcttgccc aaggcatcag aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 991  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 991

aacttcgaag ggtctgtcag aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 992  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 992

ggttgggat gatgtcaatt aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 993  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 993

taccaaagtc aggttacgtt aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 994  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 994

tgagatcagc ttggtcatg aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 995  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 995

ttggcaatgg ttcccaaatt aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 996  
<211> LENGTH: 41

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 996

ctgaagagcc tccatgaatg aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 997  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 997

ccaccaagta ggcagaataa aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 998  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 998

tgctttgtga tcacaaccac aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 999  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 999

cagaagactc ccaagcatac aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1000  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1000

agcacgcaca gtgaaggaac aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1001  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1001

tctaggtact ctgtctgatc aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1002  
<211> LENGTH: 41  
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1002

taaaggggtga tgggatagcc aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1003  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1003

tgttttagttc ttctgatca aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1004  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1004

agggtttctg gtccaaatag aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1005  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1005

tcattagtga ggctcttgta aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1006  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1006

aaagtgcttg actgccaaagt aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1007  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1007

tgaattccaa ctgaccttct aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1008  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 1008

gagcccgaag aggaataaat aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1009  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 1009

tgaacacacg gcgacatag aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1010  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 1010

atcaactcat cacagctgtc aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1011  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 1011

aagattttgc tctgctggag aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1012  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 1012

agagaagagc tcaaggcact aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1013  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 1013

gtggattcca agcttgagat aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1014  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 1014

agactgggag gtatgatagc aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 1015  
 <211> LENGTH: 41  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 1015

ctctgacaga gatgtcatct aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 1016  
 <211> LENGTH: 41  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 1016

tagatggact tctgtgtctc aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 1017  
 <211> LENGTH: 41  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 1017

gctccacaaa agctgagttg aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 1018  
 <211> LENGTH: 41  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 1018

catatatacc acctcgaagc aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 1019  
 <211> LENGTH: 41  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 1019

acacagtact cgtcaatggg aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 1020  
 <211> LENGTH: 41  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 1020

ttcccatcaa attccttgag aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1021  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1021

gagattgtca ccttctcaac aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1022  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1022

tgcagcaagg tgaagacaca aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1023  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1023

gctttttggc catcatatag aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1024  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1024

aactgcctta tcattcttgt aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1025  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1025

atcctcaagg gaaaagccag aaaaatggag tttgggcaga t 41

<210> SEQ ID NO 1026  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

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<400> SEQUENCE: 1026  
tgatcatgcg atagatgagg aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 1027  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1027  
catcaggaac tgcagcattg aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 1028  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1028  
caagggcaca agttttcaa aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 1029  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1029  
tactgccttc aacacaagga aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 1030  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1030  
agagtagaga gggaatggg aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 1031  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
probe

<400> SEQUENCE: 1031  
tacacaacat ccaatcctgc aaaaatggag ttgggcaga t 41

<210> SEQ ID NO 1032  
<211> LENGTH: 16  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
oligonucleotide

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<400> SEQUENCE: 1032

agatgacgct tgggaa 16

<210> SEQ ID NO 1033

<211> LENGTH: 22

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 1033

tcgctctctg ctctctctgt tc 22

<210> SEQ ID NO 1034

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 1034

cgccaatac gaccaaacc 20

<210> SEQ ID NO 1035

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 1035

gtcaacccca cegtgttctt c 21

<210> SEQ ID NO 1036

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 1036

tttctgctgt ctttgggacc ttg 23

<210> SEQ ID NO 1037

<211> LENGTH: 10

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 1037

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What is claimed is:

1. A method for detecting a presence of a 800 nucleotides to 2.1 kb long target nucleic acid sequence in the genome of intact mammalian cells with high efficiency and high resolution, the method comprising:

contacting the intact mammalian cells with a first plurality of probes, wherein each probe comprises a first detectable label and a probe sequence that binds to a portion of the target nucleic acid sequence; and

detecting a presence of the first detectable label localized to a region in the genome in the intact cells, wherein the presence of the first detectable label indicates the presence of the target nucleic acid sequence,

wherein the target nucleic acid is

an endogenous nucleic acid sequence present in the genome of the cells or an exogenous nucleic acid sequence integrated into the genome of the cells and is a non-amplified nucleic acid sequence;

wherein the first plurality of probes comprises probes between 30 and 50 nucleotides in length,

wherein the first plurality of probes comprises 30 probes to less than 50 probes; and

wherein the first plurality of probes are tiled across the target nucleic acid sequence upon hybridization, wherein the high efficiency comprises detection of at least half of the number of actual number of target sequences present in the cells, in at least 50% of the cells that comprise the target sequence, and

wherein high resolution comprises delineation of 800 nucleotides to 2.1 kb long target sequences separated by 4 kb intervening sequence on a chromosome.

2. The method of claim 1, further comprising: contacting the intact cells with a second detectable label that binds to a portion of a cellular structure, and

detecting a position of the first detectable label in the intact cells relative to the second detectable label, wherein the position is used to determine a spatial position of the target nucleic acid sequence.

3. The method of claim 1, wherein the intact cell are treated with RNase prior to the contacting.

4. The method of claim 1, wherein the intact cell are genetically modified cells and the method comprises genetically modifying the cells by genetic editing prior to the contacting.

5. The method of claim 1, wherein the target nucleic acid is an exogenous nucleic acid sequence, wherein the exogenous nucleic acid comprises a transgene inserted into the genome of the cells by genetic editing.

6. The method of claim 1, wherein the target nucleic acid is an endogenous nucleic acid sequence present in the genome of the cells, wherein the endogenous nucleic acid sequence is present in a DNase I hypersensitive site.

7. The method of claim 1, wherein the first detectable label comprises a fluorophore.

8. The method of claim 1, wherein the first plurality of probes comprises probes 40-50 nucleotides in length.

9. The method of claim 1, wherein the first plurality of probes comprises probes 40 nucleotides in length.

10. The method of claim 1, wherein the first plurality of probes is a set of 30 probes.

11. The method of claim 1, wherein the target sequence is 1.4 kb, 1.6 kb, or 1.8 kb in length.

12. The method of claim 11, wherein the genome of the cell is denatured at a temperature of no higher than 78° C.

13. The method of claim 12, wherein the cell is fixed with formaldehyde.

14. The method of claim 13, wherein the first plurality of probes is a set of 30 probes.

\* \* \* \* \*